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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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The present invention describes a purified Anopheles gambiae olfaction polypeptide comprising a 383, 394, 380, 411, 412, 391, 157 or 401 residue amino acid sequence (see ABP52833 to ABP52840) (S1), a conservatively modified amino acid sequence of them, or a sequence of (S1) with at least 20 consecutive residues. Also described: (1) an isolated polynucleotide comprising: (a) a nucleotide sequence encoding the purified Anopheles gambiae olfaction polypeptide; or (b) a nucleotide sequence that hybridises under stringent conditions to a hybridisation probe comprising a 1964, 1239, 1142, 1236, 1194, 1176, 474 or 1206 nucleotide sequence

New mosquito olfaction polypeptides and polynucleotides, useful for mosquito management, i.e. controlling the pest and disease vectors, for identifying pest control agents.

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Claim 18; Fig 2; 96pp; English.

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516.5	516.5	661	723	761	761	761	767.5	779.5	780	780.5	780.5	796.5	865	869.5	869.5	869.5	869.5	869.5	869.5	874	874
26.2	26.2	33.5	36.6	38.6	38.6	38.6	38.9	39.5	39.5	39.6	39.6	40.4	43.8	44.1	44.1	44.1	44.1	44.1	44.1	44.3	44.3
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Human adı	Human adı	Human pro	Pig S-ant	Human ret	Protein s	Human ret	Pig arres	Amino aci	Human pro	Cyclin-de	Amino aci	S. manson	Bacterial	Yellow tl	Green flu	Yellow tl	Rat Prote	Rat Prote		Human bet	Human bet

ALIGNMENTS

ABP52833

standard;

protein;

383

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ARRESULT 1
ARBSSIAT ARBSSIAT ARBSSIAT ARBSSIAT ARBSSIAT OL-N
XX ARSSIAT ARBSSIAT ARB
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N-PSDB; ABQ75102.
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24-JAN-2002;
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Best Local S
Matches 383
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                                                                                                                                                                                                                            Mosquito olfaction molecule, arrestin
                                                                                                                                                                                                                                                          15-JAN-2004
                                                                                                                                                                                                                                                                                                                    ABR84476 standard; protein;
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                                           08-MAR-2002; 2002US-00094240.
                                                                       10-MAR-2003;
                                                                                                       18-SEP-2003
                                                                                                                                   WO2003076590-A2
                                                                                                                                                               Anopheles gambiae
                                                                                                                                                                                             Arrestin 1; mosquito; olfaction; insecticide; antimalarial
               (UYVA-) UNIV VANDERBILT
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                                                                                                                                                                                                                                                                                                                                            standard; protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASTTLLAQPDQRDAFGVIISYAVKVKLFLGALGGELSAELPFVLMHPKPGTKAKVIHA 360
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Drosophila; developmental biology; cell signalling; insecticide;

Drosophila melanogaster polypeptide SEQ ID NO 12000

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from brosophila. The inventior useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 364 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-MAR-2000; 2000US-0191637P
11-JUL-2000; 2000US-00614150
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                                                                                                                                                                                                                                                                                                                                      PNAPSSYTLQQGEDDNGDPCGVSYYVKIFAGESETDRTHRRSTYTLGIRKIQFAPTKQGQ 180
                                                                                                                                                                                                                                                                                                                                                                                       FRYGREDDEMIGLRFQKELTLVSQQVCP-PQKQDIQLTKMQERLLKKLGSNAYPFVMQMP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MVYNFKVFKKCAPNGKVTLYMGKRDFVDHVSGVEPIDGIVVLDDEYIRDNEKVFGQIVCS
                                                                                                        CLASTTLLAQPDQRDAFGVIISYAVKVKLFLGALGGELSAELPFVLMHPKPGTKAKVIHA
                                                                                                                                                                                             VVLFQNGSYRNTVASLETSEGCPIQPGSSLQKVMYLTPLLSSNKQRRGIALDGQIKRQDQ 300
                                                                                                                                                                                                                                                                                                                  PSSPASVVLQQKASDESQPCGVQYFVKIFTGDSDCDRSHRRSTINLGIRKVQYAPTKQGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MVVNFKVFKKCSPNNMITLYMNRRDFVDSVTQVEPIDGIIVLDDEYVRQNRKIFVQLVCN
                                       EAEGSIE
                                                                      DSQADVE
                                                                                                                                                                             VVLFQNGQFRNTIAFMETSEGCPLNPGSSLQKVMYLVPTLVANCDRAGIAVEGDIKRKDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70.1%; Score 1384; I
70.3%; Pred. No. 1.80
cive 51; Mismatches
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..8e-135;
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Best Local :
                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to a polynucleotide for preventing, treating or diagnosing a disease in an individual. The composition or the polypeptide, polynucleotide or RNA precursor, or antibody is useful for diagnosing, preventing or treating diseases (e.g. cell proliferative diseases such as cancer) in an individual. These may also be used for identifying substances capable of binding to or modulating the function of the polypeptide, capable of affecting the function of the corresponding gene, or capable of inhibiting the cell division cycle or cell cycle progression, preferably mitosis and/or meiosis. The present sequence represents an antagonist of cell cycle progression protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New cell cycle progression genes and proteins for modulating cell cycle progression in cells, for preventing, treating or diagnosing cell proliferative diseases (e.g. cancer) or for identifying modulators of mitosis or meiosis.
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N-PSDB; ADQ89587.
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06-MAY-2003;
                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-OCT-2004
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                                                                                                                                                                                                                                                                                                                                      Local Similarity
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VVLFQNGSYRNTVASLETSEGCPIQPGSSLQKVMYLTPLLSSNKQRRGIALDGQIKRQDQ
                                                                                                                                                                                                                                                                     MVYNFKVFKKCAPNGKVTLYMGKRDFVDHVSGVEPIDGIVVLDDEYIRDNRKVFGQIVCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 18;
                                                                                                                                                                                                 FRYGREEDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKKLGSNAIPFTFNIS
                                                           QPCTLVRKDFMLSPGELELEVTLDKQLYLHGERIGVNICIRNNSNKAVKKIKAMVQQGVD
                                                                                                            PSSPASVVLQQKASDESQPCGVQYFVK1FTGDSDCDRSHRRSTINLGIRKVQYAPTKQGI
                                                                                                                              PNAPSSYTLQQGEDDNGDPCGVSYYVKIFAGESETDRTHRRSTYTLGIRKIQFAPTKQGQ
                                                                                                                                                                                                                                                   QPCTVVRKDFLLSPGELELEVTLDKQLYHHGEKISVNICVRNNSNKVVKKIKAMVQQGVD
                                                                                                                                                                               FRYGREDDEMIGLRFQKELTLVSQQVCP-PQKQDIQLTKMQERLLKKLGSNAYPFVMQMP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer; cell division cycle; mitosis; meiosis;
                                                                                                                                                                                                                                                                                                                        Conservative
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2003US-0468402P
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                                                                                                                                                                                                                                                                                                                                      70.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       461pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             progression
                                                                                                                                                                                                                                                                                                                      51;
                                                                                                                                                                                                                                                                                                                    Score 1384; DB 8;
Pred. No. 1.8e-135;
1; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Midgley
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RESULT 4 ADQ89588 ID ADQ8

ADQ89588 standard; protein; 364

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VVLFQNGQFRNTIAFMETSEGCPLNPGSSLQKVMYLVPTLVANCDRAGIAVEGDIKRKDT

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                                                                                                                                                                                                Query Match
Best Local S
Matches 204
                                                                                                                                                                                                                                                                                                                                                                                                          mosquito olfaction morecure. In polypeptides and the nucleic acids encoding them. These are arrestins 1 and 2 and odorant receptor molecules 1-7. The odorant receptors function in a ligand-induced signal transduction pathway for the activated signal mosquito olfaction. Arrestin functions to inhibit the activated signal transduction cascade. Thus, the odorant receptors act as an 'on' switch, and arrestin as an 'off' switch for the odorant detection system of the mosquito. Methods are provided for identifying compounds that interfere with the operation of the mosquito olfactory system, particularly compounds that modulate arrestin 2 activity. These are useful for the control of mosquitoes, particularly by reducing their ability to locate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers Misc-difference 152
                                                                                                                                                                                                                                                                                                                             Sequence 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is the protein sequence of arrestin 2, a novel mosquito olfaction molecule. The invention provides 9 novel mosquito polypeptides and the nucleic acids encoding them. These are arrestins 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 16; Fig 12b; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New mosquito arrestin 1 and 2 genes and polypeptides, useful for identifying mosquito olfaction molecule binding compounds which reduce the ability of mosquitoes to locate sources of bloodmeal, e.g. humans.
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                                                                                                                                                                                                                              Local Similarity
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                                                            MVYNFKVFKKCAPNGKVTLYMGKRDFVDHVSGVEPIDGIVVLDDEYIRDNRKVFGQIVCS
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                                                                                                                                                                                                                              51.8%; Score 1023; DB 7; 52.3%; Pred. No. 1.4e-97;
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                                                            The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL016176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
      Sequence
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Disclosure; SEQ ID NO 1314; 21pp + Sequence Listing; English
                                                       New isolated nucleic a
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N-PSDB; ABL02277.
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11-JUL-2000;
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                        The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention
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                                                                                                                                                                                                                                                                                                                NGSYRNTVASLETSEGCPIQPGSSLQKVMYLTPLLSSNKQRRGIALDGQIKRQDQCLAST
                                                                                                                                                                                                                                                                                                                                                                                                                        SVTLQPGPEDTGKACGVDYEVKAFCAENLEEKIHKRNSVRLVIRKVQYAPERPGPQPTAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SVTLQQGEDDNGDPCGVSYYVKIFAGESETDRTHRRSTVTLGIRKIQFAPTKQGQQPCTL 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EDLDVLGLTFRKDLFVANVQSFPPAPEDKKPLTRLQERLIKKLGEHAYPFTFEIPPNLPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EEDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKKLGSNAIPFTFNISPNAPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RVFKKASPNGKLTVYLGKRDFVDHIDLVDPVDGVVLVDPEYLKE-RRVYVTLTCAFRYGR
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                                                                                                                                          PVDTNLIELDTND
                                                                                                                                                                                                                                             TLLAQPDQRDAFGVIISYAVKVKLFLGALGGELSAELPFVLMHPKPGTK---AKVIHADS
                                                                                                                                                                                                                                                                                TAQYKCPVAMEEADD--TVAPSSTFCKVYTLTPFLANNREKRGLALDGKLKHEDTNLASS
                                                                                                                                                                                                                                                                                                                                                     TTRQFLMSDKPLHLEASLDKEIYYHGEPISVNVHVTNNTNKTVKKIKISVRQYADICLFN
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                                                   protein; 418
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47.2%; Pred.
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No. 1.9e-85;
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                                                                                                                                                                                                                                        The present sequence represents an arrestin protein. The specification of describes phosphorylation-independent arrestin mutants. These mutants are used in screening assays to identify ligands and/or modulators of G protein-coupled receptors (GPCRs). A method for identifying a GPCR ligand comprises contacting a composition comprising the GPCR and a constitutively active arrestin mutant with a test compound; and constitutively active arrestin mutant to modulate on modulate binding of carrestin mutant to the GPCR, where modulation of binding indicates that the test compound is a GPCR ligand. The method is used for identifying the test compound is a GPCR ligand. The method is used for identifying contential ligands and/or modulators of GPCRs, particularly modulators, for use as human therapeutics. Modulators of GPCR may be used for creating patients having e.g. retinitis pigmentosa, stationary night continuess, colour bindness, nephrogenic DI, isolated glucocorticoid deficiency, hyperfunctioning thyroid adenomas, familial hypocalciuric CC hypercalcemia, hyperparathyroidsm and heurological disorders. The methods may be used in screening assays for cidentification of gPCRs are sening assays for identification of GPCRs antagonists and/or agonists of orphan GPCRs, and for identification of GPCR antagonists and/or agonists
                                                                                                                                       Query Match
Best Local S
Matches 179
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Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying a G protein-coupled receptor ligand, useful for treating retinitis pigmentosa, color blindness or neurlogical disorders, uses phosphorylation-independent arrestin mutants particularly suited for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arrestin; phosphorylation-independent arrestin mutant; G protein-coupled receptor; GPCR; GPCR ligand; retinitis pigmentosa; stationary night blindness; colour blindness; nephrogenic D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bos sp
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                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 46; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vitro
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179; Conserv
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                                                                  KVFKKCAPNGKVTLYMGKRDFVDHVSGVEPIDGIVVLDDEYIRDNRKVFGQIVCSFRYGR
EDLDVLGLTFRKDLFVANVQSFPPAPEDKKPLTRLQERLIKKLGEHAYPFTFEIPPNLPC
                                 EEDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKKLGSNAIPFTFNISPNAPS
                                                                                                                                         Conservative
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                                                                                                                                           76;
                                                                                                                                       Score 903.5; DB 4;
Pred. No. 5e-85;
6; Mismatches 112;
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The invention relates to a complex of protein-protein interactions (forming a protein-protein interaction map, PIM) in adipocyte cells as defined in the specification, or polynucleotides in adipocyte cells as for the polypeptides. Also included are a recombinant cell expressing the interacting polypeptides and a method of selecting a modulating compound in adipocyte cells, by cultivating a recombinant host cell on a selective medium containing a modulating compound and a reporter gene the expression of which is toxic for the recombinant host cell which is transformed with two vectors, where the first vector comprises a polynucleotide encoding a first hybrid polypeptide and DNA binding domain and the second vector comprising a polynucleotide encoding a second hybrid polypeptides and an activating domain that activates the toxic reporter gene, when the first and second hybrid polypeptides interact and selecting the modulating compound which inhibits the growth of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rat; yeast two-hybrid assay; adipocyte; bait protein; NIDDM; non-insulin diabetes mellitus; obesity; selected interacting domain; SID; protein-protein interaction map; PIM; anorectic; metabolic disorder.
                                                                                                                                                                                                                                            Claim 1; Page 52;
                                                                                                                                                                                                                                                                        Novel complex of protein-protein interactions in adipocyte cells for identifying compounds that modulate the protein-protein interactions useful for treating obesity and metabolic disorders.
                                                                                                                                                                                                                                                                                                                                                                                       Legrain
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DB; ABS51031.
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                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human prey protein
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                                                                                                                                                                             11-JAN-2002;
                                                                                                                                                                                                                                   25-JUL-2002.
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Pred. No. 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          between a Shigella flexner; polypeptide (e.g. ospb) ospb1, ipaC, ipaH9.8, ospG and ospC1) and a mammalian polypeptide defined in the CC specification. The complexes are formed using the yeast two-hybrid CC system. Also included are (1) a recombinant host cell expressing the CC interactions between the Shigella flexner; polypeptide and a mammalian CC polypeptide defined in the specification; (2) selecting a modulating compound that inhibits or activates the protein-protein interactions; (3) a modulating compound obtained from the method of (2); (4) a SID CC ampound that the human polypeptide or its fragment or variant comprising the human polypeptide or its fragment or variant comprising the human polypeptides appearing as ABG7042-ABG70242; (5) a CC SID polymelectide or its fragment or variant comprising encoding the conve polypeptides a vector comprising (5); (6) a recombinant host cell CC containing the vector; and (10) a protein chip comprising Shigella CC flexneri polypeptide and a mammalian polypeptide defined in the compound, conficient or polymuclecticie is useful for treating or preventing CC shigellosis (bacillary dysentery) in a human or mammal. The present CC sequence represents a human prey protein isolated by the yeast two-hybrid assay, forming a complex of the invention with a shigella protein
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Best Local S
Matches 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New complex of protein-protein interactions between a bait Shigella flexneri polypeptide and a prey mammalian or human placenta polypeptide for treating or preventing bacillary dysentery in a mammal or human.
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                     21-OCT-2004
                                                        ADQ89786;
                                                                                            ADQ89786 standard;
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Pred. No. 1e-84;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to a polynucleotide for preventing, treating or diagnosing a disease in an individual. The composition or the polypeptide, polynucleotide or RNA precursor, or antibody is useful for diagnosing, preventing or treating diseases (e.g. cell proliferative diseases such as cancer) in an individual. These may also be used for identifying substances capable of binding to or modulating the function of the polypeptide, capable of affecting the function of the corresponding gene, or capable of finibiting the cell division cycle or cell cycle progression, preferably mitosis and/or meiosis. The present sequence represents an antagonist of cell cycle progression protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New cell cycle progression genes and proteins for modulating cell cycle progression in cells, for preventing, treating or diagnosing cell proliferative diseases (e.g. cancer) or for identifying modulators of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-544089/52.
N-PSDB; ADQ89785.
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06-MAY-2003; 2003US-0468402P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mitosis or meiosis.
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                                                                                                                                     NGSYRNTVASLETSEGCPIQPGSSLQKVMYLTPLLSSNKQRRGIALDGQIKRQDQCLAST
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                                                                                                                                                                                                                                                                                                                                                                                                                       RVFKKASPNGKLTVYLGKRDFVDHIDLVDFVDGVVLVDPEYLKE-RRVYVTLTCAFRYGR
   KVIHADSQADVETFRQDTID 375
                                       TLLREGANREILGIIVSYKVKVKLVVSRGGLLGDLASSDVAVELPFTLMHPKPKEEPPHR 363
                                                                          TLLAQPDQRDAFGVIISYAVKVKLFL--GALGGELSA----ELPFVLMHPKPGTK---A
                                                                                                               TAQYKCPVAMEEADD--TVAPSSTFCKVYTLTPFLANNREKRGLALDGKLKHEDTNLASS
                                                                                                                                                                                          TTRQFLMSDKPLHLEASLDKEIYYHGEPISVNVHVTNNTNKTVKKIKISVRQYADICLFN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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112; 8

Indels Length

Gaps

65

303 305 185

418; 13;

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364

EVPENETPVDTNLIELDTND

383

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CC describes phosphorylation-independent arrestin mutants. These mutants are CC used in screening assays to identify ligands and/or modulators of G CC protein-coupled receptors (GPCRs). A method for identifying a GPCR ligand CC comprises contacting a composition comprising the GPCR and a CC constitutively active arrestin mutant with a test compound; and CC determining the ability of the test compound to modulate binding of CC arrestin mutant to the GPCR, where modulation of binding indicates that the test compound is a GPCR ligand. The method is used for identifying CC potential ligands and/or modulators of GPCRs, particularly modulators, CC for use as human therapeutics. Modulators of GPCR may be used for treating patients having e.g. retinitis pigmentosa, stationary night CC deficiency, hyperfunctioning thyroid adenomas, familial hypocalciuric CC hypercalcenia, hyperparathyroidism and neurological disorders. The cC methods may be used for screening pluralities of test compounds (e.g. a CC small molecule library of compounds) or a composition containing a CC identification of GPCRs antagonists and/or agonists of orphan GPCRs, and for identification of GPCR antagonists and/or agonists
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G protein-coupled receptor; GPCR; GPCR ligand; retinitis pigmentosa; stationary night blindness; colour blindness; nephrogenic DI; isolated glucocorticoid deficiency; hyperfunctioning thyroid adenoma; familial hypocalciuric hypercalcemia; hyperparathyroidism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 46; 47pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying a G protein-coupled receptor ligand, useful for treating retinitis pigmentosa, color blindness or neurlogical disorders, uses phosphorylation-independent arrestin mutants particularly suited for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-602637/68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Berstein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arrestin; phosphorylation-independent arrestin mutant; gigmentosa; Grotein-coupled receptor; GPCR; GPCR ligand; retinitis pigmentosa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amino acid sequence of human beta-arrestin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                   present sequence represents an arrestin protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      screening assays.
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   45
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   . 5%
                                                                                                                                                                                                                                                                                                                                                                                                                                                      English
   Score
Pred.
   897.5; DB 4;
No. 2.1e-84;
                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                     The
                   418;
                                                                                                                                                                                                                                                                                                                                                                                                                       specification
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RESULT 14
ABG13574
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                                                                                                                                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                         The invention sequences. (I)
                                                                                                                                                                                                                                                    N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                               31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; chromosome mapping; gene mapping; gene therapy; forensic
food supplement; medical imaging; diagnostic; genetic disorder.
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                     reaction (PCR)
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DB; AAS77761.
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                                                                                                                                                                                                                                                                                                                                                        HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SVTLQQGEDDNGDPCGVSYYVKIFAGESETDRTHRRSTVTLGIRKIQFAPTKQGQQPCTL 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EEDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKKLGSNAIPFTFNISPNAPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RVFKKASPNGKLTVYLGKRDFVDHIDLVDPVDGVVLVDPBYLKE-RRVYVTLTCAFRYGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTRQFLMSDKPLHLEASLDKEIYYHGEPISVNVHVTNNTNKTVKKIKISVRQYADICLFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SVTLOPGPEDIGKACGVDYEVKAFCAENLEEKIHKRNSVRLVIRKVQYAPERPGPQPTAE 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KVIHADSQADVETFRODTID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EDLDVLGLTFRKDLFVÁNVÓSFÞPAPEDKKPLTRLÓERLIKKLGEHÁYÞFTFEI PPNLÞC 125
                                                                                                     SEQ
                                                                                                                                                                                                                                                                                                             Liu C,
                                                                                                                                                                                                                                                                                                                                                                                               2000US-00540217.
2000US-00649167.
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relates to isolated polynucleotide (I) and polypeptide (II) is useful as hybridisation probes, polymerase chain primers, oligomers, and for chromosome and gene mapping, inant production of (II). The polynucleotides are also used
                                                                                                     ij
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                                                                                                     103pp;
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                                                                                                     English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 113;
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Ś 밁 S 밁 Ś 밁 δ 밁 á 밁 Ś 밁

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RESULT 15
AAG67785
ID AAG677
XX AAG67
XX AAG67
XX AACC
DE AA ex
XX AACC
KW G pro
KW G pro
KW Statil
KW isola
KW isola
KW isola
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XX Unide
XX Unide
PN WO200
PF 05-M2
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Best Local S
Matches 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forenaics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                       Arrestin; phosphorylation-independent arrestin mutant; g protein-coupled receptor; GPCR; GPCR ligand; retinitis pigm stationary night blindness; colour blindness; nephrogenic DI; isolated glucocorricoid deficiency; hyperfunctioning thyroid familial hypocalciuric hypercalcemia; hyperparathyroidism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders
                                                                                                                                                                                                                                                                                             An exemplary phosphorylation-independent arrestin mutant.
  05-MAR-2001; 2001WO-US007304.
                                        13-SEP-2001.
                                                                              WO200167106-A2
                                                                                                                                                     neurological
                                                                                                                                                                                                                                                                                                                                   10-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                            AAG67785 standard; protein; 382
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                                                                                                                   Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ftp.wipo.int/pub/published
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAQYKCPVAMEEADD -- TVAPSSTFCKVYTLTPFLANNREKRGLALDGKLKHEDTNLASS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SVTLQQGEDDNGDPCGVSYYVKIFAGESETDRTHRRSTVTLGIRKIQFAPTKQGQQPCTL 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EEDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKKLGSNAIPFTFNISPNAPS
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                                                                                                                                                           disorder.
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48.6%; Pred. No. 1.1e-83;
tive 75; Mismatches 100
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                                                                                                                                                                                                                                    retinitis pigmentosa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents an exemplary phosphorylation-independent CC arrestin mutant. Such mutants are used in screening assays to identify C ligands and/or modulators of G protein-coupled receptors (GPCRs). A CC method for identifying a GPCR ligand comprises contacting a composition comprising the GPCR and a constitutively active arrestin mutant with a CC test compound; and determining the ability of the test compound to CC modulate binding of arrestin mutant to the GPCR, where modulation of binding indicates that the test compound is a GPCR ligand. The method is CC used for identifying potential ligands and/or modulators of GPCRs, comparison of GPCRs, where modulators of GPCR may be used for treating patients having e.g. retinitis pigmentosa, stationary night bindness, colour bindness, nephrogenic DI, isolated CI stationary night bindness, colour bindness, nephrogenic DI, isolated CI stationary in the methods may be used for screening pluralities of test compounds (e.g. a small molecule library of compounds) or a composition containing a plurality of GPCRs. The methods may be used in screening aparts of identification of natural and surrogate agonists of orphan and composition containing the identification of natural and surrogate agonists of orphan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Sim:
Matches 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 382 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying a G protein-coupled receptor ligand, useful for treating retinitis pigmentosa, color blindness or neurlogical disorders, uses phosphorylation-independent arrestin mutants particularly suited for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 47; 47pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vitro screening assays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-602637/68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-MAR-2000; 2000US-0186706P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and for identification of GPCR antagonists and/or agonists
                                                                                                                                                                           KVFKKCAPNGKVTLYMGKRDFVDHVSGVEPIDGIVVLDDEYIRDNRKVFGQIVCSFRYGR
                              TLLAQPDQRDAFGVIISYAVKVKLFLGALGGELSAELPFVLMHPKP
                                                                          TAQYKCPVAQLEQDD--QVSPSSTFCKVYTITPLLSDNREKRGLALDGKLKHEDINLASS
                                                                                                    NGSYRNTVASLETSEGCÞIQÞGSSLQKVMYLTÞLLSSNKQRRGIALDGQIKRQDQCLAST
                                                                                                                                                                                                                                                                    SVTLQQGEDDNGDPCGVSYYVKIFAGESETDRTHRRSTVTLGIRKIQFAPTKQGQQPCTL
                                                                                                                                                                                                                                                                                                                                      EEDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKKLGSNAIPFTFNISPNAPS
TIVKEGANKEVLGILVSYRVKVKLVV-SRGGDVSVELPFVLMHPKP
                                                                                                                                                       TTRHFLMSDRSLHLEASLDKELYYHGEPLNVNVHVTNNSTKTVKKIKVSVRQYADICLFS
                                                                                                                                                                                                                                  SVTLQPGPEDTGKACGVDFEIRAFCAKSLEBKSHKRNSVRLVIRKVQFAPEKPGPQPSAE
                                                                                                                                                                                                                                                                                                            EDLDVLGLSFRKDLFIATYQAFPPVPNPPRPPTRLQDRLLRKLGQHAHPFFFTIPQNLPC
                                                                                                                                                                                                                                                                                                                                                                                         RVFKKSSPNCKLTVYLGKRDFVDHLDKVDPVDGVVLVDPDYLKD-RKVFVTLTCAFRYGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 885; DB 4;
Pred. No. 3.8e-83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 382
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Search completed: May

20,

2006,

time

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence:
 pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                   1149
1135
973.5
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Gapop 10.0 , Gapext 0.5
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(without alignments)
898.805 Million cell updates/sec
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1973
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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 MVYNFKVFKKCAPNGKVTLY.....ADVETFRQDTIDQQASVDFE 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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 B
A34867
A55081
A56607
A56607
A34856
A34856
A348404
B45682
B46682
B
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                                                   hypothetical prote
arrestin isoform 1
arrestin isoform 2
cone arrestin - Af
cone arrestin - bu
cone arrestin - mouse
arrestin - human
S-antigen - rat
S-antigen - bovine
retinal S-antigen
rod arrestin - nor
                                                                                                                                                                                                                                                                       arrestin homolog -
arrestin - fruit f
arrestin 1 - blueb
arrestin homolog -
arrestin homolog -
49K photoreceptor
arrestin 2 - blueb
beta-arrestin, bra
beta-arrestin 1 - r
beta-arrestin 1 - r
beta-arrestin 1 - b
arrestin arr31 - b
arrestin - human (
arrestin isoform 1
beta-arrestin 2 -
beta-arrestin 2 -
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                  arrestin-C - hurod arrestin -
                  ' - human
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ALIGNMENTS

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Qy 361 DSQADVETFRODTIDQQASVD 381	Qy 301 CLASTTLLAQPDQRDAFGVIISYAVKVKLFLGALGGELSAELPFVLMHPKPGTKAKVIHA 360 	Qy 241 VVLFQNGSYRNTVASLETSEGCPIQPGSSLQKVMYLTPLLSSNKQRRGIALDGQIKRQDQ 300	Qy 181 QPCTLVRKDFMLSPGELELEVTLDKQLYLHGERIGVNICIRNNSNKMVKKIKAMVQQGVD 240	Qy 121 PNAPSSVTLQQGEDDNGDPCGVSYYVKIFAGESETDRTHRRSTVTLGIRKIQFAPTKQGQ 180	Qy 61 FRYGREEDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKKLGSNAIPFTFNIS 120	Qy 1 MVYNFKVFKKCAPNGKVTLYMGKRDFVDHVSGVEPIDGIVVLDDEYIRDNRKVFGQIVCS 60	Query Match 76.0%; Score 1499; DB 2; Length 381; Best Local Similarity 72.7%; Pred. No. 1.2e-110; Matches 277; Conservative 51; Mismatches 51; Indels 2; Gaps 2	A; Note : preliminary; increate and sequence and all all all all all all all all all al	ger, J.; Breer, H. Insect antennae. [D:93199955; PMID:8452755	arrestin homolog - tobacco budworm C;Species: Heliothis virescens (tobacco budworm) C;Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 09-Jul-2004 C;Date: n. R56607
						-	2;		conceptual	04

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A;Molecule type: DNA
A;Residues: 1-364 <SMI>
A;Residues: 1-364 <SMI>
A;Cross-references: UNIPROT:P15372; UNIPARC:UPI000000E69; GB:M30177
R;Hyde, D.R.; Mecklenburg, K.L.; Pollock, J.A.; Vihtelic, T.S.; Benzer, Sproc. Natl. Acad. Sci. U.S.A. 87, 1008-1012, 1990
Proc. Natl. Acad. Sci. U.S.A. 87, 1008-1012, 1990
A;Title: Twenty Drosophila visual system cDNA clones: one is a homolog of A;Reference number: A34868; MUID:90138926; PMID:2105491
A;Reference number: A34868; MUID:90138926; PMID:2105491
A;Accession: A34868
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-364 <HYDD-
A;Cross-references: UNIPARC:UPI0000000E69; GB:M30140; NID:g156961; PIDN:7
A;Genetics:
A;Genetics:
A;Genetics: FlyBase:FBgn0000120
A;Introns: 36/3; 306/3; 336/3; 336/3; 349/3
C;Superfamily: arrestin
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(;Species: Drosophila melanogaster)
C;Date: 20-Jul-190 #sequence_revision 20-Jul-1990 #text_c
C;Accession: A34867; A34868
R;Smith, D.P.; Shieh, B.H.; Zuker, C.S.
Proc. Natl. Acad. Sci. U.S.A. 87, 1003-1007, 1990
A;Title: Isolation and structure of an arrestin gene from A;Reference number: A34867; MUID:90138925; PMID:1689056
A;Accession: A34867
A;Accession: A34867
arrestin 1 - bluebottle fly (Calliphora vicina)
c;Species: Calliphora vicina
C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_
C;Accession: A55081; S44291
C;Accession: A55081; S44291
C;Accession: A56081; S44291
C;Accession: A56081; S44291
C;Accession: A56081; S44291
C;Accession: A56081; Milney, M.; Paulsen, R.
J; Biol. Chem. 269, 26969-26975, 1994
A;Title: Mechanism of arrestin 2 function in rhabdomeric
A;Reference number: A55081; MUID:95014564; PMID:7929436
                                                                                                                                                                                                      RESULT
A55081
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Matches 258
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58; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                          ALASTTLIASQDARDAFGIIVSYAVKVKLFLGALGGELCAELFFILMHFKPSRKAQL---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51;
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                                                                                                                           #text_change
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                              photoreceptors
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Cell. Signal. 5, 69-80, 1993
A; Fittle: Arrestin-subtypes in insect antennae.
A; Reference number: A56607; MUID:93199955; PMID:8452755
A; Contents: antennae
A; Contents: A56607
A; Status: preliminary
A; Status: preliminary
A; Status: preliminary
                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 1-407 <RAM>
A;Cross-references: UNIPROT:P32122; UNIPARC:UPI000012608B; GB:S57174; NID:g298755; PIDN:I
A;Note: sequence extracted from NCBI backbone (NCBIN:127923, NCBIP:127925)
C;Superfamily: arrestin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: A55081
A;Status: preliminary
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-363 <PLA>
A;Residues: 1-363 <PLA>
A;Cross-references: UNIPROT:P51486; UNIPARC:UPI0000126075; GB:X79072; NID:g483527;
A;Note: the source is designated as Calliphora erythrocephala
C;Superfamily: arrestin
                                                                                                                                                                                                                                                                                                                                                                                                                  arrestin homolog - migratory locust (Species: Locusta migratoria (migratory locust) (C;Species: Locusta migratoria (migratory locust) (C;Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 09-Jul-2004 (C;Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 09-Jul-2004 (C;Accession: A5607 ); Krieger, J.; Breer, H. (Cell. Signal. 5, 69-80, 1993
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                                                        EEDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKKLGSNAIPFTFNISPNAPS
                                                                                                     SLASTTLIASQEARDAFGIIVSYAVKVKLFLGALGGELCAELPFILMHPKPSLKA-----
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 SVTLQQGEDDNGDPCGVSYYVKIFAGESETDRTHRRSTVTLGIRKIQFAPTKQGQQ-PCT
                                  EEDEVMGLKFTKEMVLAKEQIVPQ-TKEKMELTPIQERLMKKLGPNAFPFTFHFPASSPS
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Pred. No. 9.8e-98;
7; Mismatches 55
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arrestin homolog - fruit fly (Drosophila miranda)
C;Species: Drosophila miranda
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S11566
R;Krishnan, R.; Ganguly, R.
Nucleic Acids Res. 18, 5894, 1990
Nucleic Acids Res. 18, 5894, 1990
A;Title: Nucleotide sequence of the arrestin-like 49 Kd protein gene of Dros A;Reference number: S11566; MUID:91016944; PMID:2216789
A;Accession: S11566
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A;Introns: 286/1; 351/1
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                                                                            QCLASTTLLAQ-PDQRDAFGVIISYAVKVKLFLGALGGELSAELPFVLMHPKPGT-----
                                                                                                              EITMV-NAQFSKHVAQLETKEGCPITPGANLTKTFYLIPLAANNKDRHGIALDGHLKDED
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R;Plangger, A.; Malicki, D.; Whitney, M.; Paulsen, R.
J. Biol. (Chem. 269, 2696-26975, 1994
A;Title: Mechanism of arrestin 2 function in rhabdomeric photoreceptors.
A;Reference number: A55081; MUID:95014564; PMID:7929436
A;Accession: B55081
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-401 <PLA>
A;Residues: 1-401 <PLA>
A;Rotoss-references: UNIPROT:P51487; UNIPARC:UPI000016B8DC; EMBL:X79073; NID:g483583; PID
A;Note: the source is designated as Calliphora erythrocephala
C;Superfamily: arrestin
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A;Title: A 49-kilodalton phosphoprotein in the Drosophila photoreceptor A;Reference number: A34856; MUID:90232360; PMID:2158671
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C;Date: 13-Jul-1990 #sequence_revision
                                                                                                                                                                                                                                        arrestin 2 - bluebottle fly (Calliphora vicina)
C;Species: Calliphora vicina
C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change
C;Accession: B55081; S44292
C;Accession: B55081; S44292
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A;Cross-references: FlyBase:FBgn0000121
C;Superfamily: arrestin
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A;Residues: 1-401 <YAM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 48.5
90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q-PCTLVRKDFMLSPGELELEVTLDKQLYLHGERIGVNICIRNNSNKMVKKIKAMVQQGV 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MVYNFKVFKKCAPNGKVTLYMGKRDFVDHVSGVEPIDGIVVLDDEYIRDNRKVFGQIVCS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DVVLFQNGSYRNTVASLETSEGCPIQPGS9LQKVMYLTPLLSSNKQRRGIALDGQIKRQD 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VNLASSTMVQEGKSTGDACGIVISYSVRIKLNCGTLGGEMQTDVPFKLLQPAPGTIEKKR 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QCLASTTLLAQ-PDQRDAFGVIISYAVKVKLFLGALGGELSAELPFVLMHPKPGT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RLPSSLVSKGFTFSNGKISLEVTLDREIYYHGEKTAATVQVSNNSKKSVKSIKCFIVQHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PNSPSSVTLQQEGDDNGKPLGVEYTIRAFVGDSEDDRQHKRSMVSLVIKKLQYAPLNRGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PNAPSSYTLOOGEDDNGDPCGVSYYVKIFAGESETDRTHRRSTVTLGIRKIQFAPTKQGQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRYGREEDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKKLGSNAIPFTFNIS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MVVSVKVFKKATPNGKVTFYLGRRDFIDHIDYCDPVDGVIVVEPDYLK-NRKVFGQLATT
                                                                                                                                                                                                                                                                                                                                                                                                                        SNAMKKMKSIEQHRNVKGYYQDDDDNIVFEDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---KAKVIHADSQADVETFRODTIDQQASVDF 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EITMV-NAQFSKHVAQLETKEGCPITPGANLTKTFYLIPLAANNKDRHGIALDGHLKDED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 975.5; DB 2
Pred. No. 2.7e-69;
'4; Mismatches 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UNIPARC: UPI0000126081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-Jul-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kobayashi, H.; Sakai, Y.; Hotta, Y.; Matsumoto,
                                                                                                                                                                                                                                                                                                                                                                                                                            389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   401;
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Query Match

47.8%;

Score

942.5;

В

<u>۷</u>

Length

401;

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C;Specias: Bob primigenius taurus (cattle)
C;Specias: Bob primigenius taurus (cattle)
C;Colate: 13 Jul-1990 #sequence_revision 21-Oct-1992 #text_change 09-Jul-2004
C;Accession: A34851; JC2052
R;Lohae, M.J.; Benovic, J.L.; Codina, J.; Caron, M.G.; Lefkowitz, R.J.
Science 248, 1547-1550, 1990
A;Title: Beta-arrestin: a protein that regulates beta-adrenergic receptor function.
A;Reference number: A34851; MUJD:90296080; PMID:2163110
A;Accession: A34851
A;Accession: A34851
A;Residues: 1-418 <LOHs
A;Residues: 1-418 <LOHs
A;Cross-references: UNIPROT:P17870; UNIPARC:UPI0000042307; GB:M33601; NID:g162691; PIDN:
A;Experimental source: brain
R;Sterne-Marr, R; Gurevich, V.V.; Goldsmith, P.; Bodine, R.C.; Sanders, C.; Donoso, L.A
J;Biol. Chem. 268, 1540-15648, 1993
A;Title: Polypeptide variants of beta-arrestin and arrestin3.
A;Reference number: A47140; MUID:93340166; PMID:8340388
A;Accession: JC2052
A;Status: nucleic acid sequence not shown
A;Residues: 1-15, 'C',17-30,'L',32,'K',34-83,'Y',85-176,'K',178-206,'L',208-333,342-418 <
A;Cross-references: UNIPARC:UPI00001788C1
A;Cross-references: UNIPARC:UPI00001788C1
A;Experimental source: lung, spleen
C;Comment: This protein is an arrestin homolog which acts analogously to desensitize the F;1-419/Product: beta-arrestin, brain #status predicted <MAT>
F;1-333,342-418/Product: beta-arrestin, brain #status predicted <MAZ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           beta-arrestin, brain - bovine
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                                                                                                                                                                              Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 Q-PCTLVRKDFMLSPGELELEVTLDKQLYLHGERIGVNICIRNNSNKMVKKIKAMVQQGV
                                                                                                                                                           179;
                         99
                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---KAKVIHADSQADVETFRQDTIDQQASVDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DVVLFQNGSYRNTVASLETSEGCPIQPGSSLQKVMYLTPLLSSNKQRRGIALDGQIKRQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RLPSSLVSKGFTFSNGKISLEVTLDREIYYHGGKVAATVQINNNSKKAVKNIKVFIIQHT
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EEDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKKLGSNAIPFTFNISPNAPS 125
                                                                                           KVFKKCAPNGKVTLYMGKRDFVDHVSGVEPIDGIVVLDDEYIRDNRKVFGQIVCSFRYGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QCLASTTLLAQ-PDQRDAFGVIISYAVKVKLFLGALGGELSAELPFVLMHPKPGT-----
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                                                                    RVFKKASPNGKLTVYLGKRDFVDHIDLVEPVDGVVLVDPEYLKE-RRVYVTLTCAFRYGR
                                                                                                                                                         Conservative
                                                                                                                                                                              45.8%;
                                                                                                                                                         76;
                                                                                                                                                       Score 903.5; DB 2
Pred. No. 1.4e-63;
76; Mismatches 112
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0; Mismatches 122;
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B43404
beta-arrestin1 - rat
C;Species: Rattus nor
C;Date: 27-Apr-1993 #
C;Accession: B43404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:P29066; UNIPARC:UPI0000126079; GB:M91589; A;Note: sequence extracted from NCBI backbone (NCBIP:112791) C;Superfamily: arrestin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Status: preliminary, not compared with conceptual translation A,Molecule type: nucleic acid A,Residues: 1-418 <ATT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004 C;Accession: B43404 R;Actramadal, H.; Arriza, J.L.; Aoki, C.; Dawson, T.M.; Codina, J.; Kwatra, M.M.; J. Biol. Chem. 267, 17882-17890, 1992 A;Title: Beta-arrestin2, a novel member of the arrestin/beta-arrestin gene family. A;Reference number: A43404; MUID:92388146; PMID:1517224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                VRKDEMLSPGELELEVTLDKQLYLHGERIGVNICIRNNSNKMVKKIKAMVQQGVDVVLFQ 245
                                                                                                                                                                                                                                                                                                                                                                                                       SVTLQQGEDDNGDPCGVSYYVKIFAGESETDRTHRRSTVTLGIRKIQFAPTKQGQQPCTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KVFKKCAPNGKVTLYMGKRDFVDHVSGVEBÌDGIVVLDDEYIRDNRKVFGQIVCSFRYGR
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                                                                                                                                                                                                     TAQYKCPVAMEEADD--TVAPSSTFCKVYTLTPFLANNREKRGLALDGKLKHEDTNLASS
                                                                                                                                                                                                                                                                                            TTRQFLMSDKPLHLEASLDKEIYYHGEPISVNVHVTNNTNKTVKKIKISVRQYADICLFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EEDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKKLGSNAIPFTFNISPNAPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RVFKKASPNGKLTVYLGKRDFVDHIDLVDFVDGVVLVDPEYLKE-RRVYVTLTCAFRYGR
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                           EVPESETPVDTNLIELDTND
                                                                    KVIHADSQADVETFRQDTID 375
                                                                                                                TLLREGANREILGIIVSYKVKVKLVVSRGGLLGDLASSDVAVELPFTLMHPKPKEEPPHR
                                                                                                                                                         TLLAQPDQRDAFGVIISYAVKVKLFL--GALGGELSA----BLPFVLMHPKPGTK---A
                                                                                                                                                                                                                                                                                                                                                                                   SVTLOPGPEDTGKACGVDYEVKAFCAENLEEKIHKKNSVRLVIRKVOYAPERPGPOPTAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 903.5; DB 2; ; Pred. No. 1.4e-63; 78; Mismatches 111;
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A;Cross-references: UNIPARC:UPI000016A58A; GB:L04685; NID:g347956; PIDN:AAA35558.1; A;Note: sequence extracted from NCBI backbone (NCBIP:134015) C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N;Contains: beta-arrestin 1, splice form B
(;Species: Homo sapiens (man)
(;Species: Homo sapiens (man)
(;Date: 22-Sep-1993 #sequence_revision 22-Sep-1993 #text_change 09-Jul-2004
(;Accession: B46682; A46682
(;Accession: B46682; A46682
J. Biol. Chem. 268, 9753-9761, 1993
J. Biol. Chem. 268, 9753-9761, 1993
A;Reference number: A46682; MUID:93252853; PMID:8486659
A;Accession: B46682
A;Accession: B46682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: not compared with conceptual translation A;Molecule type: mRNA A;Residues: 1-418 <PAR1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Map position: 11q13-11q13
C;Superfamily: arrestin
C;Keywords: alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT: D49407; UNIPARC: UPI000016A589; GB:L04685; NID:g347956; A;Note: sequence extracted from NCBI backbone (NCBIP:134014) A;Accession: A46682
arrestin arr3L - bovine
N;Contains: arrestin arr3S
C;Species: Bos primigenius taurus (cattle)
C;Date: 16-Feb-1994 #sequence revision 27-Jun-1994 #text_change 09-Jul-2004
C;Date: 16-Feb-1994 #sequence Tevision 27-Jun-1994 #text_change 09-Jul-2004
C;Accession: A47140; B47140; D7C2051
R;Sterne-Marr, R.; Gurevich, V.V.; Goldsmith, P.; Bodine, R.C.; Sanders, C.
R;Sterne-Marr, R.; Gurevich, V.V.; Goldsmith, P.; Bodine, R.C.; Sanders, C.
J. Biol. Chem. 268, 15640-15648, 1993
                                                                                                                                                    RESULT 11
A47140
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A; Residues: 1-333,342-418 < PAR2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VRKDFMLSPGELELEVTLDKQLYLHGERIGVNICIRNNSNKMVKKIKAMVQQGVDVVLFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SVTLQQGEDDNGDPCGVSYYVKIFAGESETDRTHRRSTVTLGIRKIQFAPTKQGQQPCTL 185
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Pred. No. 1.2e-62;
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RESULT 12
S18984
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F;1-420/Product: arrestin arr3L #status predicted <MAT>
F;1-362,374-420/Product: arrestin arr3S #status predict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-362,374-420 <ST2>
A;Cross-references: UNIPARC:UPI0000178BC3
C;Comment: This protein plays a role in the regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Experimental source: brain
A,Note: sequence extracted from NCBI backbone
A,Accession: B47140
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A;Residues: 1-420 <STE>
A;Cross-references: UNIPROT:P32120; UNIPARC:UPI0000178BC2; GB:L14641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Polypeptide variants of beta-arrestin and arrestin3. A;Reference number: A47140; MUID:93340166; EMID:8340388. A;Accession: A47140
                                                                                                                                 A;Molecule type: mRNA
A;Residues: 1-409 <RAP>
A;Cross-references: UNIPROT:P32121;
C;Superfamily: arrestin
                                                                                                                                                                                                                                                                                                            arrestin - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence
C;Accession: S18984
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В
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A;Status: preliminary
                                                                                                                                                                                                                                      A; Reference number: S18984
                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, A;Description: Isolation of a novel
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167; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SYTLOOGEDDNGDPCGVSYYVKIFAGESETDRTHRRSTVTLGIRKIQFAPTKQGQQPCTL 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EDLDVLGLSFRKDLFIANYQAFPPTPNPPRPPTRLQERLLRKLGQHAHPFFFTIPQNLPC 126
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                     KVFKKCAPNGKVTLYMGKRDFVDHVSGVEPIDGIVVLDDEYIRDNRKVFGQIVCSFRYGR
   RVFKKSSPNCKLTVYLGKRDFVDHLDKVDPVDGVVLVDPDYLKD-RKVFVTLTCAFRYGR
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                                                                      76;
                                                                  Score 882; DB 2;
Pred. No. 6.7e-62;
6; Mismatches 99;
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Pred. No. 2.8e-62;
                                                                                                                                                                                                                                                            November 1991
cDNA belonging
                                                                                                                                                         UNIPARC: UPI000016A58B;
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       99
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99

BEDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKKLGSNAIFFTFNISPNAPS 125

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arrestin isoform 1S, erythrocyte - rainbow trout C;Species: Oncorhynchus mykiss (rainbow trout) C;Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004 C;Accession: S68253 R;Jahns, R.; Borgese, F.; Lindenthal, S.; Straub, A.; Motais, R.; Fievet, B. Biochem. J. 316, 497-506, 1996 A;Title: Trout red blood cell arrestin (TRCarr), a novel member of the arrest A;Reference number: S68253; MUID:96257743; PMID:8687393 A;Accession: S68253 A;Occession: S68253; MUID:96257743; PMID:8687393 A;Accession: S68253; Mulcleic acid sequence not shown
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S68253
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A; Residues: 1-407 < JAH>
A; Cross-references: UNII
C; Superfamily: arrestin
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C;Species:
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beta-arrestin
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                                                                                                                                                                                                                                                                                                                                                                                               VRKDFMLSPGELELEVTLDKQLYLHGERIGVNICIRNNSNKYVKKIKAMVQQGVDVVLFQ 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SVTLQQGEDDNGDPCGVSYYVKIFAGESETDRTHRRSTVTLGIRKIQFAPTKQGQQPCTL
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                     N
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                                                                                                                                                                                                                                                                                          TAQYKCPVAQVEADD -- QVSSSSTFCKVYTLTPTLDKNREKRGLALDGKLKHEDTNLASS
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                                                                                                                                                               SQADVET --- FRQDTIDQQASVDFE 383
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                                                                                                                          SDPPIDTNLIEFETNSFSQDDDFVFE
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(Norway
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  R;Bradshaw, H.; Gattung, S. submitted to the EMBL Data Library, November 1995 A;Description: The sequence of C. elegans cosmid F53H8 A;Reference number: Z21501 A;Accession: T34297
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hypothetical protein F53H8.2 - Caenorhabditis elegans

Species: Caenorhabditis elegans;Date: 29-Oct-1999 #sequence_revision;Accession: T34297

29-Oct-1999 #text_change 21-Jan-2000

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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-320, 'A', 322-325, 'A', 327-330, 'A', 332-410 <ATZ>
A; Residues: 1-320, 'A', 322-325, 'A', 327-330, 'A', 332-410 <ATZ>
A; Rote: sequence: UNIPARC:UPI0000178BC5; GB:M91590; NID:g949986
A; Note: sequence is revised in GenBank entry RATBARRESZ, release 113.
R; Craft, C.M.; Whitmore, D.H.; Wiechmann, A.F.
J. Biol. Chem. 269, 4613-4619, 1994
A; Title: Come arrestin identified by targeting expression of a functional A; Reference number: 154423; MUID:94140898; PMID:8308033
A; Accession: 170112
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 295-410 <CRA>
A; Cross-references: UNIPARC:UPI0000170BB4; EMBL:U03627; NID:g458202; PID: C; Superfamily: arrestin
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J. Biol. Chem. 267, 17882-17890, 1992
A;Title: Beta-arrestin2, a novel member of the arrestin/beta-arrestin gene family.
A;Reference number: A43404; MUID:92388146; PMID:1517224
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R;Attramadal, H.; Arriza, J.L.; Aoki, C.; Dawson, T.M.; Codina, submitted to GenBank, August 1995
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A; Residues: 1-410 < ATT>
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A; Accession: A59279
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                              TTLLAQPDQRDAFGVIISYAVKVKLFLGALGGELSAELPFVLMHPKP
                                                                                                                                       QNGSYRNTVASLETSEGCPIQPGSSLQKVMYLTPLLSSNKQRRGIALDGQIKRQDQCLAS
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                                                                                            STAQYKCPVAQLEQDD--QVSPSSTFCKVYTITPLLSDNREKRGLALDGQLKHEDTNLAS
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Pred. No. 6.5e-61
6; Mismatches 9
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-454 <BRA>
A;Cross-references: UNIPARC:UPI0000178BC6; EMBL:U41023; PIDN:AAA82342.1; CESP:F53H8.2
C;Genetics:
Search completed: May 20, 2006, 22:48:27 Job time: 42 secs
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;Gene: CESP:F53H8.2
;Introns: 11/2; 61/1; 155/3; 189/2; 237/3; 290/2; 338/2; 389/3; 416/2
;Superfamily: arrestin
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O4R562_MACFA
O48752_MOUSE
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P51486 calliphora
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Q7q5q8 drosophila
P51102 drosophila
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P51104 drosophila
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
Anophelinae; Anopheles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21819361; PubMed=11792843; DOI=10.1073/pnas.022505499; Merrill C.E., Riesgo-Escovar J., Pitts R.J., Kafatos F.C., Carlson J.R., Zwiebel L.J.;
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GO; GO:0007165; P:signal transduction; I
InterPro; IPR000698; Arrestin_C.
InterPro; IPR011022; Arrestin_C.
InterPro; IPR011021; Arrestin_N.
PANTHER; PTHR11792; Arrestin_T.
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Pfam; PF00339; Arrestin_N; 1.
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07-FEB-2006, entry version 17
                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21184354; PubMed=11287006; DOI=10.1016/S0014-5793(01)02287-6; Bentrop J., Schillo M., Gerdon G., Draslar G., Paulsen R.; "UV-light-dependent binding of a visual arestin 1 isoform to photoreceptor membranes in a neuropteran (Ascalaphus) compound eye."; FEBS Lett. 493:112-116(2001).
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta;
Neoptera; Endopterygota; Neuroptera; Ascalaphidae;
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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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InterPro; IPR000698; Arrestin.
InterPro; IPR011022; Arrestin_C.
InterPro; IPR011021; Arrestin_N.
PANTHER; PTHR11792; Arrestin_T.
Pfam; PF02752; Arrestin_C; 1.
Pfam; PF00339; Arrestin_N; 1.
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P55274;
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noc!
Noctuidae; Heliothinae; Heliothis.
NCBI_TaxID=7102;
                                                                                                                                                                                                                                                                                                                                                             MEDLINE=9319995; PubMed=8452755; DOI=10.1016/0898-6568(93)90009-Raming K., Freitag J., Krieger J., Breer H.; "Arrestin-subtypes in insect antennae."; Cell. Signal. 5:69-80(1993).
                                                                                                                                                                                                                                                                                                 Copyrighted
Distributed
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  Sensory transduction
                     PRINTS; PR00309; ARRESTIN. ProDom; PD002099; Arrestin; PROSITE; PS00295; ARRESTINS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Antenna;
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                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE, AND TISSUE SPECIFICITY.
MEDIJUS=90138925; PubMed=1689056;
Smith D.P., Sheih B.-H., Zuker C.S.;
"Isolation and structure of an arrestin gene fro proc. Natl. Acad. Sci. U.S.A. 87:1003-1007(1990)
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Gall Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Hender George R.A., Lewis S.E., Richards S., Ashburner M., Hender Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L. Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfei
                                              STRAIN=Berkeley;
MEDLINE=20196006;
Adams M.D., Celni)
                                                                                                                     MEDLINE=90138926; PubMed=2105491;
Hyde D.R., Mecklenburg K.L., Pollock J.A., Vihtelic
"Twenty Drosophila visual system cDNA clones: one is
human arrestin.";
                                                                                                                                                                                                                                                                                                                                                                         ARRA DROME STANDARD; PRT; 364 AA.
P15372; Q9VJAB;
01-APR-1990, integrated into UniProtKB/Swiss-Prot.
01-APR-1990, sequence version 1.
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                                                            PubMed=10731132; DOI=10.1126/science.287.5461.2185
                                                                                                            Sci. U.S.A. 87:1008-1012(1990)
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RA Beeson K.Y., Banos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
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RA Borkova D., Botchan M.R., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davemport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA docton K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McDeod M.P., McPherson D.L.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., McPherson D.L.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puti V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Syler E., Spradling A.C., Stapleton M., Skupski M.P., Shith T.,
RA Syler E., Spradling A.C., Stapleton M., Skupski M.P., Shith T.,
RA Syler E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Yelson B. R., Myers E.W., Rubin G.M., Venter J.,
RN (1918) S., Zhounce of Drosophila melanogaster.";
RN (2018) S., Zhounce of Drosophila melanogaster.";
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Staple Ton B.A., Guarin H.,
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Beeson K.Y.,
                                                                                            MEDLINE=93303590; PubMed=8316831; Dolph P.J., Ranganathan R., Colley Zuker C.S.;
                                                                                                                                                                                                                                     Matsumoto H., Yamada T. "Phosrestins I and II:
                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22426066; PubMed=12537569;
                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Berkeley;
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                                   rhodopsin in vivo.";
Science 260:1910-1916(1993)
                                                                                                                                                                                  Biochem.
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                                                                         "Arrestin function
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                                                                                                                                                                                                                                                                                       bin G.M., Celniker S.E.;
bin G.M., Celniker S.E.;
Drosophila full-length cDNA resource.";
"orme Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002)
 FUNCTION: Regulates photoreceptor cell proteins are mediators of rhodopsin in
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- ^^^6069; PubMed=12537572;
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Benos P.V., Berman B.P., Bhandari D., Bolshakov
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                                                                                                                                                                                                                    phosphorylation
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-J., Andrews-Pfannkoch C., Baldwin D.,
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GO; GO:0016028; C:rhabdomere; IDA.
GO; GO:0016028; C:rhabdomere; IDA.
GO; GO:0016060; F:protein binding; IPI.
GO; GO:0016060; P:metarhodopsin inactivat:
InterPro; IPR000698; Arrestin.
InterPro; IPR011022; Arrestin_N.
InterPro; IPR011021; Arrestin_N.
PANTHER; PTHR11792; Arrestin; 1.
Pfam; PF02752; Arrestin_C; 1.
Pfam; PF03339; Arrestin_N; 1.
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Ensembl; CG5711; Drosophila
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PIR; A34867; A34867.
HSSP; P17870; 1G4M.
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BioCyc; DMEL-XXX-02:DMEL-XXX-02-009314-MONOMER;
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QSVIMG: CGG10949; NbExp=1; IntAct=EBI-145156, EBI-186540;
QSVAP2: CG11881; NbExp=1; IntAct=EBI-145156, EBI-186540;
QSVAP2: CG31545; NbExp=1; IntAct=EBI-145156, EBI-190361;
QSVEP0: CG3754; NbExp=1; IntAct=EBI-145156, EBI-190361;
QSVEP0: CG3995; NbExp=1; IntAct=EBI-145156, EBI-160250;
QSVEP0: CG3995; NbExp=1; IntAct=EBI-145156, EBI-186076;
QSVTHS: CG6175; NbExp=1; IntAct=EBI-145156, EBI-125350;
QSVTHS: CG6254; NbExp=1; IntAct=EBI-145156, EBI-125350;
QSVTHS: CG6254; NbExp=1; IntAct=EBI-145156, EBI-125350;
QSVTHS: CG6175; NbExp=1; IntAct=EBI-145156, EBI-125350;
QSVTHS: CG6254; NbExp=1; IntAct=EBI-145156, EBI-125350;
QSVTHS: CG6254; NbExp=1; IntAct=EBI-145156, EBI-125350;
QSVTHS: CG6254; NbExp=1; IntAct=EBI-145156, EBI-160250;
QSVTHS: CG6254; NbExp=1; IntAct=EBI-145156, EBI-160250;
QSVTHS: CG6175; Nb
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SIMILARITY: Belongs
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M30140; AAA28380.1; -; Genomic_DNA.
AE003657; AAF55844.1; -; Genomic_DNA.
AE061824; AAF27635.1; -; mRNA.
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CLASTILLAQPDORDAFGVIISYAVKVKLFLGALGGELSAELPFVLMHPKPGTKAKVIHA
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                                                                                                        VVLFQNGQFRNTIAFMETSEGCPLNPGSSLQKVMYLVPTLVANCDRAGIAVEGDIKRKDT
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                                                                                                                                                                                                                                         QPCTVVRKDFLLS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51;
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Pred. No. 2.6e
51; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               melanogaster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /FTId=PRO_0000205215.
0DCC764C4F890FC2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phosrestin-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inactivation;
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c_DNA.
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                                                                                                                                                                                                                                             /RNNSNKVVKKI KAMVQQGVD
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RESULT 6
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Best Local (
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InterPro; IPR011021; Arrestin_N.
PANTHER; PTHR11792; Arrestin; 1.
Pfam; PF02752; Arrestin_C; 1.
Pfam; PF00339; Arrestin_N; 1.
PFANTS; PR00309; ARRESTIN.
PRODOm; PD002099; ARRESTIN; 2.
PROSCITE; PS00295; ARRESTIN; 1.
PROSCITE; PS00295; ARRESTIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ARR1 CALVI
P51486;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Calliphora vicina (Blue blowfly) (Calliphora erythrocephala).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
Calliphoridae; Calliphora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A55081; A55081.
HSSP; P17870; 1G4M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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Name=ARR1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sensory transduction; Vision. CHAIN 1 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X79072; CAA55672.1; -; mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plangger A., Malicki D., Whitney M., Paulsen R.;
"Mechanism of arrestin 2 function in rhabdomeric photoreceptors.
"Biol. Chem. 269:26969-26975(1994).
-!- SIMILARITY: Belongs to the arrestin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95014564;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE [MRNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=7373;
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240
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                                                                                                                                                                                                                                                                                                         MVYNFKVEKKCAPNGKVTLYMGKRDFVDHVSGVEPIDGIVVLDDEYIRDNRKVFGQIVCS
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                                                                                                                                                                                                                                                         FRYGREEDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKKLGSNAIPFTFNIS
                          QPCTLVRKDFMLSPGELELEVTLDKQLYLHGERIGVNICIRNNSNKMVKKIKAMVQQGVD
                                                                                                                                                      PSSPASVVLQQKANDSTQPCGVQYFVKVFAGENDCDRSHRRSTVNLGIRKVQYAPTKTGI
                                                                                                                                                                        PNAPSSVTLQQGEDDNGDPCGVSYYVKIFAGESETDRTHRRSTVTLGIRKIQFAPTKQGQ
                                                                                                                                                                                                                                FRYGREDDEMIGLRFOKELILVSQPVYPE-QKIDIQLTKMQERLLKKLGSNAYPFILEMP
                                                                            QPCTVVRKDFLLSPGELELEVTLDRQLYYHGEKISINICVRNNSNKVVKKIKAMVQQGID
  VVLFQNGQFRNTIAFAESSEGCPLNPGSSLQKIMYLVPNLAANCDRAGIAVEGDVKHKNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                               363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entry version 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          integrated into UniProtKB/Swiss-Prot
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                                                                                                                                                                                                                                                                                                                                                                                                       67.7%; Score 1335; DB 1; Length 363; 67.4%; Pred. No. 1.8e-96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               40680 MW;
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/FTId=PRO_0000205214.
; 7C345D818E46C23E CF
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Best Local Similarity
Matches 245; Conserv
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EMBL; AY333992; AAR01117.1; -; G

EMBL; AY333993; DAR01118.1; -; G

EMBL; AY333995; DAR01120.1; -; G

EMBL; AY333995; DAR01121.1; -; G

EMBL; AY333996; DAR01129.1; -; G
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NON TER
SEQUENCE
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05-JUL-2004, sequence versi
07-FEB-2006, entry version
Arrestin (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0007600; P:sensory perception; 1
GO; GO:0007165; P:signal transduction;
GO; GO:0007165; P:signal transduction;
InterPro; IPR0100598; Arrestin_C.
InterPro; IPR011022; Arrestin_C.
PANTHER; PTHR11792; Arrestin_C; 1.
Pfam; PF02752; Arrestin_C; 1.
PRINTS; PR00309; ARRESTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q6VPP0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PD002099;
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                                                                                                                                                                                              DFMLSPGELELEVTLDKQLYLHGERIGVNICIRNNSNKMVKKIKAMVQQGVDVVLFQNGS
                                                                                                                                                                                                                        DFMLSPGELELEVTLDKQLYLHGERIGVNICIRNNSNKWVKKIKAMVQQGVDVVLFQNGS
                                                                                                                                                                                                                                                                                                   LQQGEDDNGDPCGVSYYVKIFAGESETDRTHRRSTVTLGIRKIQFAPTKQGQQPCTLVRK
        FRODT 373
                                                                  aqpdqrdafgviisyavkvklflgalggelsaelpfvlmhpkpgtkakvihadsqadvet
                                                                                                                                          YRNTVASLETSEGCPIQPGSSLQKVMYLTPLLSSNKQRRGIALDGQIKRQDQCLASTTLL
                                                                                                                                                                                                                                                                           LQQGEDDNGDPCGVSYYVKIFAGESETDRTHRRSTVTLGIRKIQFAPTKQGQQPCTLVRK
                                            AQPDQRDAFGVIISYAVKVKLFLGALGGELSAELPFVLMHPKPGTKAKVIHADSQADVET
                                                                                                                      YRNTVASLETSEGCPIQPGSSLQKVMYLTPLLSSNKQRRGIALDGQIKRQDQCLASTTLL
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245 ‡
                                                                                                                                                                                                                                                                                                                                                   63.6%; Score 1254; DB 2; ilarity 100.0%; Pred. No. 2.6e-90; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              integrated into UniProtKB/TrEMBL
sequence version 1.
entry version 9.
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IEA.
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245;

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Gaps

368 180

240

120 248 60

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Anopheles gambiae (African malaria mosquito).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
Anophelinae; Anopheles.
                                                                                     STRAIN=4aRR, Yaounde, and L3-5; Morlais I., Poncon N., Simard F., Cohuet A., Fontenille Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
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Matches 233
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PRODOM; PD002099; ARRESTINS; 1
PROSITE; PS00295; ARRESTINS; 1
NON TER 1
NON TER 269 269
SEQUENCE 269 AA; 30553 MW;
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Submitteed (APR-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry w
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Eukaryota; Metazoa; Arthropoda; He
Neoptera; Endopterygota; Diptera;
Anophelinae; Anopheles.
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07-DEC-2004, integrated into UniProtKB/TrEMBL.
07-DEC-2004, sequence version 1.
07-FEB-2006, entry version 7.
ENSANGP00000027511 (Fragment).
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InterPro; IPR011021; Arrestin_N.
PANTHER; PTHR11792; Arrestin; 1.
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"Anopheles gambiae re-
Submitted (APR-2002) t
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Q5TNW2_ANOGA
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                                                                                                                                                                                                                   97
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                                        QPCTLVRKDFMLSPGELELEVTLDKQLYLHGERIGVNICIRNNSNKMVKKIKA
                                                                                                                                                                                                                                                FRYGREEDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKKLGSNAIPFTFNIS 120
                                                                                                                                                                                                                                                                                                                                                          MVYNFKVFKKCAPNGKVTLYMGKRDFVDHVSGVEPIDGIVVLDDEYIRDNRKVFGQIVCS
                                                                                                                                                    PNAPSSVTLQQGEDDNGDPCGVSYYVKIFAGESETDRTHRRSTVTLGIRKIQFAPTKQGQ 180
                                                                                                                                                                                                                                                                                                                             MVYNFKVFKKCAPNGKVTLYMGKRDFVDHVSGVEPIDGIVVLDDEYIRDNRKVFGQIVCS
QPCTLVRKDFMLSPGELELEVTLDKQLYLHGERIGVNICIRNNSNKMVKKIKA
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.larity 100.0%;
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ARRESTINS; 1.
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2) to the EMBL/GenBank/DDBJ databases.
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; Pred. No. 1.7e-87;
0; Mismatches 0;
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a; Nematocera; Culicoidea; Culicidae;
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269
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Best Local S
Matches 191
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QTQ2V9; 
15-DEC-2003, integrated into UniProtKB/TrEMBL. 
15-DEC-2003, sequence version 1. 
07-MAR-2006, entry version 15. 
ENSANGP00000004989 (Kurtz arrestin-like prote: 
Name=ARRK; ORFNames=ENSANGG00000003863;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-23159591; PubMed=14986925; DOI=10.1046/j.1365-2583.2003.00450.x; MOITIL C.E., Pitts R.J., Zwiebel L.J.; Merrill C.E., Pitts R.J., Zwiebel L.J.; "Molecular characterization of arrestin family members in the malaria vector mosquito, Anopheles gambiae."; Insect Mol. Biol. 12:641-650(2003).
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PRODOM; PD002099; ARRESTINS; 2.
PROSITE; PS00295; ARRESTINS; 1.
NON TER
1
SEQÜENCE 431 AA; 47810 MW;
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GO; GO:0007165; P:signal transduction;
Interpro; IPR000698; Arrestin.
Interpro; IPR011022; Arrestin C.
Interpro; IPR011021; Arrestin N.
PANTHER; PTHR11792; Arrestin; 2.
Pfam; PF02752; Arrestin C; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Copyrighted by the UniProt Consortium, see http://www.uniprot.org/.co
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neoptera; Endopterygota;
Anophelinae; Anopheles.
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Pfam; PF00339; Arrestin_
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VRKDFMLSPGBLELEVTLDKQLYLHGERIGVNICIRNNSNKMVKKIKAMVQQGVDVVLFQ
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                                                                                SVSLOPAPGDTGKPCGVDYELKAFVGESQEDKPHKRNSVRLAIRKIMYAPSKLGEQPSIE
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                                                                                                                                                                                                                                                                                                                                                                                    52.5%; Scc
54.1%; Pro
tive 75;
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                                                                                                                                                                                                                                                                                                                                                                                          Score 1036; DB 2;
Pred. No. 8.2e-73;
5; Mismatches 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85C110785A815916 CRC64;
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GO; GO:0007660; P:sensory perception; IEA.
GO; GO:0007165; P:sensory perception; IEA.
GO; GO:0007165; P:sensory perception; IEA.
InterPro; IPR01020; Arrestin C.
InterPro; IPR011021; Arrestin N.
PANTHER; PTHR11792; Arrestin N.
PANTHER; PTHR11792; Arrestin N.
PFGam; PF00339; Arrestin N; 1.
Pfam; PF00339; Arrestin N; 1.
PFAM; PF00399; Arrestin N; 1.
PRINTS; PR00309; ARRESTIN.
PROSITE; PS00299; ARRESTIN.
PROSITE; PS00299; ARRESTINS; 1.
SEQUENCE 398 AA; 44536 MW; 73DD73FB34F014.
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QTQ5Q8; Q66GU6;
QTQ5Q8; Q66GU6;
15-DEC-2003, integrated into UniProtKB/TrEMBL.
QT-DEC-2004, sequence version 2.
QT-MAR-2006, entry version 14.
QT-MAR-2006, entry version 2.
QT-MAR-2006, entry versio
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Merrill C.E., Pitts R.J., Zwiebel L.J.;
"Molecular characterization of arrestin family members in the malaria vector mosquito, Anopheles gambiae.";
Insect Mol. Biol. 12:641-650(2003).
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Submitted (APR-2002)
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   61
                                                                                                                                                                                                              Similarity
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                                                                                                              MYNFKVFKKCAPNGKVTLYMGKRDFVDHVSGVEPIDGIVVLDDEYIRDNRKVFGQIVCS
   FRYGREEDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKKLGSNAIPFTFNIS
                                                                MVVAVKVFKKSAPNGKLTVYLGKRDF1DHTDYCDP1DGV1VLDEEYLR-GRKVFGQL1TT
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                                                                                                                                                                                  Conservative
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                                                                                                                                                                                  65;
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                                                                                                                                                                                                           Score 1023;
Pred. No. 7.
                                                                                                                                                                                                                                                                                                       73DD73FB34F01418 CRC64;
                                                                                                                                                                               Mismatches 111;
                                                                                                                                                                                                              DB 2;
.8e-72;
                                                                                                                                                                                                                                          Length
                                                                                                                                                                                  Indels
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RESULT 11
Q9V393_DROME
                                                                                                                                                                                           RA Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Addams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davemport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davemport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Wei M.-H., Ibegwam C.,
RA Harris N.L., Harvey D.A., Heiman T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Meison D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Mount S.M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Reinert K., Renington K., Saunders R.D.C., Scheele M.G.,
RA Reinert N., Renese M.G., Sampson M., Skupski M.P., Smith T.,
Spier E., Spier E., Spier E., Spier E., Tector u., Svirskas R., Tector u., Svirskas R., Wassarman D.A., W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CG1487-PA (Kurtz arrestin) (LD31082p).
Name=krz; ORFNames=CG1487, Dmel_CG1487;
Drosophila melanogaster (Fruit fly).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Q9V393;
                                                                                                       Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith:
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VIHADSQADVETFRODT---IDQQASVDFE 383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=10731132; DOI=10.1126/science.287.5461.2185;
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                                                                                                                                                                                Smith T.,
                                                                                                              Wang
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Weinstock G.M., Weissenbach J.,

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Berkeley Drosophila Genome Pro
Celniker S., Carlson J., Wan K
Hoskins R., Stapleton M., Pacl.
Yu C., Rubin G.,
"Drosophila melanogaster releat
Submitted (MAR-2000) to the EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.

MEDLINE=22426065; PubMed=12537568;

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George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
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                                                                            Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., I George R., Gonzalez M., Guarin H., Kronmiller B., Li P., I Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rul
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S. Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
MEDLINE=22426070; PubMed=12537573;
MEDLINE=22426070; PubMed=12537573;
Medlinker J.S., Bergman C.M., Kronmiller
Patel S., Frise E., Wheeler D.A., Lewis
Ashburner M., Celniker S.E.;
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                                                                   George R., Gonzalez M., Miranda A., Mungall C.J. Patel S., Phouanenavong Celniker S.;
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Drosophila."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The transposable elements of the Drosophila melanog a genomics perspective.";
Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
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                                                                                                                                                 STRAIN=Berkeley;
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MEDLINE=20341329; Pu
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MEDLINE=22426069; PubMed=12537572;
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R., Smith E.
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FlyBase; FBgn0040206; krz.
FlyBase; FBgn0040206; krz.
GO; GO:0005515; F:protein binding;
GO; GO:000515; F:protein circlestin.
InterPro; IPR011022; Arrestin.
InterPro; IPR011021; Arrestin.
InterPro; IPR011021; Arrestin.
InterPro; IPR011022; Arrestin.
InterPro; IPR011022; Arrestin.
InterPro; IPR011021; Arrestin.
InterPro; IPR011029; Arrestin.
InterPro; PR00339; Arrestin.
InterPro; PR00339; Arrestin.
InterPro; PR00399; ARRESTINS; 1.
R PRINTS; PR00309; ARRESTINS; 1.
R PROSITE; PS00295; ARRESTINS; 1.
R PROSITE; PS00295; ARRESTINS; 1.
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ARRH LOCMI STANDARD;

P32122;

01-OCT-1993, integrated into

01-OCT-1993, sequence versio

07-FEB-2006, entry version 3
                                                                                                                                                                                                                                                                                                                                  Arrestin homolog.
Locusta migratoria (Migratory locust).
Eukaryota; Metazoa; Arthropoda; Hexapoda;
Neoptera; Orthopteroidea; Orthoptera; Cae.
Acridoidea; Acrididae; Oedipodinae; Locusi
    EMBL;
PIR; A
                                                                                                                                MEDLINE=93199955; PubMed=8452755; DOI=10.1016/0898-6568(93)90009-Raming K., Freitag J., Krieger J., Breer H.; "Arrestin-subtypes in insect antennae."; Cell. Signal. 5:69-80(1993).

-i- SIMILARITY: Belongs to the arrestin family.
                                                                    Copyrighted
Distributed
                                                                                                                                                                                                                                                TISSUE=Antenna;
                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                              NCBI_TaxID=7004;
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C P19107; Q9VSN6;
C P19107; Q9VSN6;
T 01-NOV-1990, integrated into UniProtKB/Swiss-Prot.
T 24-MAY-2004, sequence version 2.
T 07-FEB-2006, entry version 54.
E Phosrestin-1 (Phosrestin I) (Arrestin B) (Arrestin-2) (49 kDa arrestin-1ike protein).
E Arrestin-1ike protein).
N Name=Arr2; Synonyms=ArrB; ORFNames=CG5962;
N Name=Arr2; Synonyms=ArrB; ORFNames=CG5962;
C Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; C Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; C Endopterygota; Drosophila.
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InterPro; IPR011022; Arrestin C.
InterPro; IPR011021; Arrestin N.
PANTHER; PTHR11792; Arrestin; 1.
Pfam; PF00752; Arrestin C; 1.
Pfam; PF00339; Arrestin N; 1.
PRINTS; PR00309; ARRESTIN.
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                                                                                                                                                         NUCLEOTIDE SEQUENCE (GENOMIC DNA).
MEDLINE-90232360; PubMed=2158671;
MEDLINE-7-Frenchi Y., Kmoroi N.,
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                              Science 248:483-486(1990)
[2]
  NUCLEOTIDE SEQUENCE
                                                                                                                                      Matsumoto
                                                                                         49-kilodalton phosphoprotein restin homolog.";
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  [LARGE SCALE GENOMIC DNA]
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RA Adams M.D., Celniker S.E., Holt R.A., KNANS C.A., Galle R.F.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Ballew R.M., Basu A., Baxendale J., Bayrakrarglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayrakrarglu L., Beasley E.M.,
RA Burtis K.C., Besus A., Baxendale J., Bayrakrarglu L., Beasley E.M.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
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RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dawnes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Cherry J.M., Cawley S., Dawnes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Cherry J.M., Cawley S., Dawnes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
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RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Howland T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Liang Y., Liai Z.,
Liang Y., Liai Z.,
Liang Y., Liai Z.,
RA Welmon D.R., Welson K.A., Naxon K., Nusskern D.R., Neiben H.,
RA Welmon D.R., Welson K.A., Naxon K., Nusskern D.R., Smith T.,
RA Welmon D.R., Welson K.A., Sanders R.D.C., Scheeler F., S
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Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.
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Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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                                                                                           MEDLINE=94242441; PubMed=8185954; DOI=10.1016/0896-6273(94)90309-3; Matsumoto H., Kurien B.T., Takagi Y., Kahn E.S., Kinumi T., Komori Yamada T., Hayashi F., Isono K., Pak W.L.; "Phosrestin I undergoes the earliest light-induced phosphorylation a calcium/calmodulin-dependent protein kinase in Drosophila
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                                     Neuron 12:997-1010(1994).
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                                                                                                                                                                                                                                               Biochem.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  "Annotation of the Drosophila melanogaster euchromatic genome: a systematic review.";
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SPECIFICITY: Inner and outer segments,
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Y., Kahn E.S., Kinumi T., Komori
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EMBL; M32141; AAA28833.1; -; Genomic_DNA.

DR EMBL; AE003554; AAF50380.1; -; Genomic_DNA.

DR HIS; A14856; A34856.

DR HSSP; P17870; 1164M.

DR Ensembl; CG5962; Drosophila melanogaster.

F1yBase; FBgn0000121; Arr2.

DR BioCyc; DMEL-XXX-02-DBEL-XXX-02-DFB.

GO; GO:0005624; C:membrane fraction; IDA.

DR GO; GO:0016028; C:rhabdomere; IDA.

GO; GO:0016028; C:soluble fraction

R GO; GO:0016029; F:metarh-~

R GO; GO:0016062; P:metarh-~

R GO; GO:0016062; P:metarh-~

R GO; GO:0016062; P:metarh-~
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PRODOM; PD002099; ARRESTIN; 2.

PROSTIE; PS00295; ARRESTINS; 1.

Complete proteome; Phosphorylation; Sensory transduction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPRO00698; Arrestin.
InterPro; IPRO11022, Arrestin C.
InterPro; IPRO11021, Arrestin N.
PANTHER; PTHR11792; Arrestin; 1.
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GO:0016028; C:rhabdomere; IDA.
GO:0016025; C:soluble fraction; IDA.
GO:0016030; F:metarhodopsin binding; TAS.
GO:0016062; P:adaptation of rhodopsin mediated
GO:0016060; P:metarhodopsin inactivation; IMP.
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                                                                                                                                                                                                                                                                                                             DVVLFQNGSYRNTVASLETSEGCPIQPGSSLQKVMYLTPLLSSNKQRRGIALDGQIKRQD
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                                                                                                                                                                                          VNLASSTMVQEGKSTGDACGIVISYSVRIKLNCGTLGGEMQTDVPFKLLQPAPGTIEKKR
                                                                                                                                                                                                                                                                                                                                                                                                                                       PNSPSSVTLQQEGDDNGKPLGVEYTIRAFVGDSEDDRQHKRSMVSLVIKKLQYAPLNRGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MVVSVKVFKKATENGKVTFYLGRRDFIDHIDYCDEVDGVIVVEPDYLK-NRKVFGQLATT
                                                                                                          SNAMKKMKSIEQHRNVKGYYQDDDDDNIVFEDF
                                                                                                                                                 --- KAKVIHADSQADVETFRODTIDQQASVDF
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109
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401 AA;
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    STANDARD;
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109
111
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48.7%;
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Pred. No. 1.
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/FTId=PRO_0000205217
    PRT;
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-> H (in Ref. 1).
12C776E0DA8F0D87 CRC64;
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    401
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    B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CaMK).
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Best Local S
Matches 190
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01-NOV-1990, integrated into UniProtKB/Swiss-Prot.
01-NOV-1990, sequence version 1.
07-FEB-2006, entry version 41.
Phosrestin-1 (Phosrestin I) (Arrestin B) (Arrestin Phosrestin-1 (Phosrestin I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic Acids Res. 18:5894-5894(1990).
-!- FUNCTION: Undergoes light-induced phosphorylation, an important role in the photoreceptor transduction.
-!- TISSUE SPECIFICITY: Inner and outer segments, and in plexiform regions of the retina.
-!- SIMILARITY: Belongs to the arrestin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=Arr2; Synonyms=ArrB;
Drosophila miranda (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Brachycera; Muscc
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00309; ARRESTIN.
ProDom; PD002099; Arrestin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X54084; CAA38019.1; -; Genomic_DNA.
PIR; S11566; S11566.
HSSP; P17870; 1G4M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Krishnan R., Ganguly "Nucleotide sequence Drosophila miranda."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProDom; PD002099; Arrestin; 2. PROSITE; PS00295; ARRESTINS; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interpro; IPR000698; Arrestin.
Interpro; IPR011022; Arrestin.V.
Interpro; IPR011021; Arrestin.V.
PANTHER; PTHR11792; Arrestin; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Phosphorylation; Sensory transduction; Vision.
CHAIN 1 401 Phosrestin-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF02752; Arrestin_C; 1.
Pfam; PF00339; Arrestin_N; 1.
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                                                                                                                                                                                                                                                        PNAPSSVTLQQGEDDNGDPCGVSYYVKIFAGESETDRTHRRSTVTLGIRKIQFAPTKQGQ
                                                                                                                                                                                                                                                                                                                                                        FRYGREEDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKKLGSNAIPFTFNIS
                                                                                                                                                                                                                                                                                                                                                                               MVVSVKVFKKATĖNGKVTFYLGRRDFIDHLDYCDEVDGVIVVEPEYLK-NRKVFGQLATT
                                                                                                                                                                                                                                                                                                                                                                                                                                       MVYNFKVFKKCAPNGKVTLYMGKRDFVDHVSGVEPIDGIVVLDDEYIRDNRKVFGQIVCS
                                                                    EITMV-NAOFSKHVAOLETKEGCPITPGANLTKTFYLIPLAANNKDRHGIALDGHLKDED
                                                                                                        DVVLFQNGSYRNTVASLETSEGCPIQPGSSLQKVMYLTPLLSSNKQRRGIALDGQIKRQD
                                                                                                                                                                                                                                                                                                                 YRYGREEDEVMGVKFSKELILSRDEIVPM-TNPNMEMTPMQEKLVRKLGSNAHPFTFHFP
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of the arrestin-like
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 977.5; DB 1;
Pred. No. 3e-68;
6; Mismatches 113;
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/FTId=PRO_000020521
; E46EEBC2485AF99C
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GO; GO:0007165; P:signal transduction; IEA.
InterPro; IPR001029; Arrestin_C.
InterPro; IPR011022; Arrestin_N.
PANTHER; PTHR11792; Arrestin; 1.
Pfam; PF02752; Arrestin_C; 1.
Pfam; PF02752; Arrestin_C; 1.
Pfam; PF00339; Arrestin_N; 1.
PRINTS; PR00309; ARRESTIN;
PROSITE; PR00309; ARRESTINS; 1.
SEQUENCE 390 AA; 43802 MW; 492250C466COEE
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12-APR-2005,

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12-APR-2006,

07-FEB-2006,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stapleton M., Carlson J., Chavez C., Frise E., George R. Park S., Wan K., Yu C., Rubin G.M., Celniker S.; Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;
Neoptera; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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CLASTTLLAQ-PDQRDAFGVIISYAVKVKLFLGALGGELSAELPFVLMHPKPGT-----
                                                                                                                                          VVLFQNGSYRNTVASLETSEGCPIQPGSSLQKVMYLTPLLSSNKQRRGIALDGQIKRQDQ
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Search completed: May 20, 2006, 22:43:02 Job time: 304 secs

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Maximum Match 100%
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Score
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1: /EMC Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*

7: /EMC_Celerra_SIDS3/ptodata/2/iaa/BcCOMB.pep:*
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US-09-270-767-44161
US-09-270-767-44161
US-09-569-037-4
US-09-543-681A-8172
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Sequence 24829, A	Sequence 2, Appli	Sequence 2, Appli	Sequence 43701, A	Sequence 4536, Ap		Sequence 867, App		Sequence 19232, A	Sequence 2, Appli	Sequence 775, App	Sequence 775, App	Sequence 775, App	Sequence 775, App		Sequence 775, App	Sequence 775, App	Sequence 775, App	Ď

ALIGNMENTS

g &	DЬ	Qy	Qy Db	Db Qy	Qy db	dd VQ	Query Match Best Local Matches 17	RESULT 1 US-09-880-137 Sequence 3, Patent No. Patent No. GENERAL INF ADPLICANT: TITLE OF 11 FILE REFER: CURRENT APPL CURRENT FILE PRIOR FILL! PRIOR FILL! PRIOR FILL! PRIOR FILL! PRIOR FILL! PRIOR FILL! SOFTWARE: SOFTWARE: SEQ ID NO 3 LENGTH: 4 TYPE: PRI ORGANISM: US-09-880-137
306 TLLAQPDQRDAFGV11SYAVKVKLFLGALGGBLSAELEFFLMHFKAFGIK-"-AKVIRHOS 304 : : : : : ::	246 TAQYKCPVAMEEADDTVAPSSTFCKVYTLTPFLANNREKRGLALDGKLKHEDTNLASS 303	246 NGSYRNTVASLETSEGCPIQPGSSLQKVMYLTPLLSSNKQRRGIALDGQIKRQDQCLAST 305	186 VRKDFMLSPGELELEVTLDKQLYLHGERIÖVNICIRNNSNKMVKKIKAMVQQGVDVVLFQ 245	126 SVTLQQGEDDNGDÞCGVSYYVKIFAGESETDRTHRRSTVTLGIRKIQFAPTKQGQQPCTL 185	66 EEDEVMGLNFOKELCLASEQIYPRPEKSDKEQTKLQERLLKKLGSNAIPFTFNISPNAPS 125 :	6 KVFKKCAPNGKYTLYMGKRDFVDHVSGVEPIDGIVVLDDEYIRDNRKVFGQIVCSFRYGR 65	y Match 46.0%; Score 907.5; DB 2; Length 410; Local Similarity 47.2%; Pred. No. 6.6e-87; hes 176; Conservative 78; Mismatches 112; Indels 7; Gaps 4;	US-09-880-137-3 US-09-880-137-3 Sequence 3, Application US/09880137 Sequence 3, Application US/09880137 Patent No. 6640025 PATENTIANT: Berstein, Gabriel APPLICANT: Berstein, Gabriel TITLE OF INVENTION: METHODS OF ASSAYING FOR G TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS FILE REFERENCE: MNI-131 CURRENT APPLICATION NUMBER: US/09/880,137 CURRENT FILING DATE: 2001-03-05 PRIOR APPLICATION NUMBER: US 60/186,706 PRIOR FILING DATE: 2000-03-03 NUMBER OF SEQ ID NOS: 8 SOFTWARE: FastSEQ for Windows Version 4.0 LENGTH: 410 TYPE: PRT ORGANISM: Homo sapiens US-09-880-137-3

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363 QADVETFRODTID 375

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; Sequence 2, Application US/09880137
PALERI NO. 6640025
; GENERAL INFORMATION:
APPLICANT: Berstein, Gabriel
TITLE OF INVENTION: METHODS OF ASSAYING FOR G
TITLE OF INVENTION: METHODS OF ASSAYING FOR G
TITLE OF INVENTION: MITHODS OF ASSAYING FOR G
TITLE OF INVENTION: MUTHOR US/09/880,137
CURRENT APPLICATION NUMBER: US/09/880,137
CURRENT APPLICATION NUMBER: US/09/880,137
CURRENT FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: US/09/86,706
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 8
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CURRENT APPLICATION NUMBER: US/09/880,137

CURRENT FILING DATE: 2001-03-05

PRIOR FILING DATE: 2000-03-03

PRIOR FILING DATE: 2000-03-03

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1

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; TYPE: PRT
; ORGANISM: Bos taurus
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US-09-880-137-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 45.8%;
Best Local Similarity 47.1%;
Matches 179; Conservative
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; Pred. No. 1.8e-86; 
76; Mismatches 112;
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RECEPTOR LIGANDS
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; TYPE: PRT
; ORGANISM: Homo
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APPLICANT: Berstein, Gabriel
APPLICANT: Berstein, Gabriel
TITLE OF INVENTION: METHODS OF ASSAYING FOR G
TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
FILE REFERENCE: MNI-131
CURRENT FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: US/09/880,137
CURRENT FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: US 60/186,706
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 382
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LENGTH: 418
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Best Local
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                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: Homo sapiens
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167; Conserv
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                                                  KVIHADSQADVETFRODTID 375
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48.3%;
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                                                                                                                Score 885; DB 2;
Pred. No. 1.4e-84;
7; Mismatches 98
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Pred. No. 7.8
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US-09-880-137-4
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Best Local Similarity
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TITLE OF INVENTION: METHODS OF ASSAYING FOR G
TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
FILE REFERENCE: MNI-131
CURRENT APPLICATION NUMBER: US/09/880,137
CURRENT FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: US 60/186,706
PRIOR APPLICATION NUMBER: US 60/186,706
PRIOR PILING DATE: 2000-03-03
NUMBER OF SEO ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 4.0
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TYPE: PRT
ORGANISM: Homo sapiens
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                                  TLLAQPDQRDAFGVIISYAVKVKLFLGALGGELSAELPFVLMHPKP 351
                                                                                                           NGSYRNTVASLETSEGCPIQPGSSLQKVMYLTPLLSSNKQRRGIALDGQIKRQDQCLAST 305
                                                                                                                                             TTRHFLMSDRSLHLEASLDKELYYHGEPLNVNVHVTNNSTKTVKKIKVSVRQYADICLFS
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 TAQYKCPVAQLEQDD--QVSPSSTFCKVYTITPLLSDNREKRGLALDGKLKHEDTNLASS
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48.3%; Pred. No. 1.6e-84;
ative 77; Mismatches 98; Indels
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RESULT 6
US-09-880-137-7
; Sequence 7, Application US/09880137
; Patent No. 6640025

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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT ETLING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,756
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
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THER INFORMATION: Description of Artificial Sequence: Homo
US-09-880-137-7
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APPLICANT: Berstein, Gabriel
APPLICANT: INVENTION: METHODS OF ASSAYING FOR G
TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
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                                                        SOFTWARE: FastSEQ for Windows Version SEQ ID NO 8383
LENGTH: 401
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CURRENT APPLICATION NUMBER: US/09/880,137
CURRENT FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: US 60/186,706
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEO ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
ORGANISM: Human
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Pred. No. 5.3e-84;
77: Mismatches 99;
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Sequence 8384, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSITITE OF INVENTION: WITH HUMAN DISEASE, METHODS OF FILE REFERENCE: CL001307

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08
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Matches
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 8384
LENGTH: 401
TYPE: PRT
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Best Local Similarity
Matches 170; Conserv
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Best Local Similarity
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                                                                                                                                          GDPCGVSYYVKIFAGESETDRTHRRSTVTLGIRKIQFAPTKQGQQPCTLVRKDFMLSPGE 196
                                                                                         KELCLASEQIYPRPEKSDKEQTKLQERLLKKLGSNAIPFTFNISPNAPSSVTLQQGEDDN 136
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                                                                      KDLFVANVQSFPPAPEDKKPLTRLQERLIKKLGEHÄYPFTFEIPPNLFCSVTLQPGPEDT 119
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GKACGVDYEVKAFCAENLEEKIHKRNSVRLVIRKVQYAPERPGPQPTAETTRQFLMSDKP
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46.1%; Pred. No. 3.3e-81;
tive 75; Mismatches 111;
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Pred. No. 3.3e-81;
Pred. Mismatches 111;
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APPLICANT: Berstein, Gabriel
TITLE OF INVENTION: METHODS OF ASSAYING FOR G
TITLE OF INVENTION: METHODS OF ASSAYING FOR G
TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR 1
FILE REFERENCE: MNI-131
CURRENT APPLICATION NUMBER: US/09/880,137
CURRENT APPLICATION NUMBER: US/09/880,137
CURRENT FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: US 60/186,706
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 8
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
SEQ ID NO 6
LENGTH: 388
TYPE: PAT
ORGANISM: Homo sapiens
US-09-880-137-6
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US-09-880-137-6
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RESULT
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Best Local (
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Local Similarity 42.7%; Pred. No. 1.6e-73;
hes 166; Conservative 79; Mismatches 125;
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                                                                                                                                                                                                                                                                                                                                                                                                                         DDLEVIGLTFRKDLYVQTLQVVPAESSSPQGALTVLQERLLHKLGDNAYPFTLQMVTNLP
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                                                                                       IHADSQADV---ETFRQDTIDQQASVDFE
                                                                                                                                                               TTLLAQPDQRDAFGVIISYAVKVKLFL--GALGGELSA----ELPFVLMHPKPGTKAKV
                                                                                                                                                                                                    SLDKYTKTVFIQEFTE--TVAANSSFSQSFAVTPILAASCQKRGLALDGKLKHEDTNLAS
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                                                       ----SSEDIVIEEFTRKGEEESQKAVEAE
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184 121 124 13 65 AND MODULATORS

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US-09-880-137-5

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; LENGTH: 388
; TYPE: PRT
; ORGANISM: Homo s
US-09-880-137-5
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-30
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9940
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CURRENT FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: US 60/186,706
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
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APPLICANY: BEZSEEIN, Gabriel
TITLE OF INVENTION: METHODS OF ASSAYING FOR G
TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR
FILE REFERENCE: MNI-131
FILE REFERENCE: MNI-131
                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
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Patent No. 6640025
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; ORGANISM: Drosophila melanogaster
US-09-270-767-58832
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                                                                                                                 US-09-270-767-43475
Sequence 43475, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins
FILE REFERENCE: File Reference: 7326-094
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Best Local Similarity
Matches 145; Conserv
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SEQ ID NO 58832
LENGTH: 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
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ORGANISM: Human
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                                                                                                                                                                                                                          295 ΙΚΑΟΦΟCLASTTLLAOPDORDAFGVIISYAVKVKLFLGA--LGGELSAELPFVLMHPKP 351
                                                                                                                                                                                                                                                                                                  235 VOQGVDVVLFQNGSYRNTVASLETSEGCPIQPGSSLQKVMYLTPLLSSNKQRRGIALDGQ
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49.6%; Pred. No. 6.6e-25;
tive 25; Mismatches 33
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; Pred. No. 2.7e-72;
66; Mismatches 88
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CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILLING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 43475
LENGTH: 475
TYPE: PRT
ORGANISM: Drosophila melanogaster
FEATURE:
FEATURE:
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APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 32381

LENGTH: 137

TYPE: PRT

ORGANISM: Drosophila melanogaster

US-09-270-767-32381
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US-09-270-767-47598
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                Sequence 47598, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
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Best Local S
Matches 52
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Patent No. 6703491
GENERAL INFORMATION:
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les 52; Conservative
NO 47598
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.4%; Score 225; DB 2; Length 137; 42.6%; Pred. No. 1.5e-15; tive 26; Mismatches 38; Indels
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SEQ ID

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; TYPE: PRT ; ORGANISM: Drosophila melanogaster US-09-270-767-47598
Search completed: May Job time : 29 secs
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                                                        136 AP 137
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                                                                                                                                                                       19 RVYKKTSPNCVLTLYLPTREIT--LTGNNPSVLRGIVYVDPKAIQGYR-VYAQLTLTFRY
                                                                                                                                64 GREEDEVMGLNFQKELCLASEQIYPRPEKSDKEQ-TKLQERLLKKLGSNAIPFTFNISPN 122
                                                                                                                76 GREDEEVMGLRFCNEAIMSLHQIWPRLEEPTPESLSPLQEALMKRLGDGAHPFTLSLSSY 135
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              20,
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42.6%;
              2006, 22:52:44
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Pred. No. 1.5e-15;
6; Mismatches 38
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Total number of hits satisfying chosen parameters:
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1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*
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Maximum Match 100%
Listing first 45 summaries
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US-09-880-137-2
US-10-043-887-348
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Sequence 2, Appli
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APPLICANT: ZWIEBEL, LAURENCE J.
FILE REFERENCE: N8289
CURRENT APPLICATION NUMBER: US/10/094,240
CURRENT APPLICATION NUMBER: 10/056,405
PRIOR APPLICATION NUMBER: 10/056,405
PRIOR APPLICATION NUMBER: 60/264,649
PRIOR FILING DATE: 2001-01-26
PRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 383
TYPE: PRT
ORGANISM: Anopheles gambiae
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                                              CLASTTLLAQPDQRDAFGVIISYAVKVKLFLGALGGELSAELPFVLMHPKPGTKAKVIHA
                                                                                                              VVLFQNGSYRNTVASLETSEGCPIQPGSSLQKVMYLTPLLSSNKQRRGIALDGQIKRQDQ
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US-09-800-137A-5
US-09-800-137A-5
US-10-722-357-31
US-10-106-998-4673
US-11-097-143-3639
US-11-097-143-3657
US-09-864-761-45375
US-09-864-761-40768
US-09-864-761-45375
US-10-945-678-16
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Sequence 36375, Ap
Sequence 3657, Ap
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Scoring table: Sequence: Perfect score:

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Sequence 2, Application US/10056405

Publication No. US20030166013A1

GENERAL INFORMATION:
APPLICANT: ZWIEBEL, LAURENCE J.

ITTLE OF INVENTION: MOSQUITO OLFACTORY GENES, POLYPEPTIDES, AND
ITTLE OF INVENTION: USE THEREOF

FILE REFERENCE: N7841

CURRENT APPLICATION NUMBER: US/10/056,405

CURRENT FILING DATE: 2002-01-24

PRIOR APPLICATION NUMBER: 60/264,649

PRIOR FILING DATE: 2001-01-26

NUMBER OF SEQ ID NOS: 23

SOFUMARE: PAtentin Ver. 2.1

SEQ ID NO 2

LENGTH: 383

TYPE: PRT
ORGANISM: Anopheles gambiae
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              Sequence 238, Application US/10954778

Publication O. US20050153368A1

GENERAL INFORMATION:

APPLICANT: ZWIEBEL, LAURENCE J.

TITLE OF INVENTION: METHOD OF IDENTIFYING CHEMICAL AGENTS WHICH STIMULATE

TITLE OF INVENTION: ODDRANT RECEPTORS OF SENSORY NEURONS

FILE REFERENCE: N1125

CURRENT APPLICATION NUMBER: US/10/954,778

CURRENT APPLICATION NUMBER: 10/056,405

PRIOR APPLICATION DATE: 2002-01-24

PRIOR APPLICATION DATE: 2002-01-24

PRIOR FILING DATE: 2002-01-24
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PRIOR APPLICATION NUMBER: 60/264,649
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; PRIOR FILING DATE: 2001-01-26; NUMBER OF SEQ ID NOS: 248; SOFTWARE: PATENTIN VEr. 3.3; SEQ ID NO 238; LENGTH: 383; TYPE: PRT; ORGANISM: Anopheles gambiae US-10-954-778-238
                                                                                                                            APPLICANT: COLORED Limited
APPLICANT: Glover, David
APPLICANT: Bell, Graham
APPLICANT: Bell, Graham
APPLICANT: Midgley, Carol
TITLE OF INVENTION: Cell Cycle Progression Proteins
FILE REFERENCE: P015819W0 CYK
CURRENT APPLICATION NUMBER: US/10/745,237
CURRENT APPLICATION NUMBER: US/10/745,237
CURRENT FILING DATE: 2003-01-0
PRIOR APPLICATION NUMBER: US 60/439,123
PRIOR APPLICATION NUMBER: US 60/439,123
PRIOR APPLICATION NUMBER: US 60/468,402
PRIOR APPLICATION NUMBER: US 60/468,402
PRIOR FILING DATE: 2003-05-06
NUMBER OF SEQ ID NOS: 600
SOFTWARE: Patentin version 3.1
SEQ ID NO 18
LENGTH: 364
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; OTHER INFORMATION: GI:7298421 US-10-745-237-18
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Best Local Similarity
Matches 383; Conserv
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Publication No. US20050227301A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                      ORGANISM: Drosophila melanogaster FEATURE: OTHER INFORMATION: AAF53644
                                                                                                                   TYPE: PRT
                                      FEATURE:
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100.0%; Pred. No. 6e-176;
ative 0; Mismatches
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Query Match

70.1%;

Score 1384;

BB .. u

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APPLICANT: VENTER: J. Craig

APPLICANT: et al.

APPLICANT: et al.

TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: DROSOPHILA GENES.

TITLE OF INVENTION: DROSOPHILA GENES.

TITLE OF INVENTION: DROSOPHILA GENES.

CURRENT APPLICATION NUMBER: US/11/097,143

CURRENT FILING DATE: 1999-10-05

PRIOR APPLICATION NUMBER: 60/157,832

PRIOR FILING DATE: 1999-10-19

PRIOR APPLICATION NUMBER: 60/160,191

PRIOR APPLICATION NUMBER: 60/161,932

PRIOR APPLICATION NUMBER: 60/164,769

PRIOR APPLICATION NUMBER: 60/164,769

PRIOR APPLICATION NUMBER: 60/173,383

PRIOR APPLICATION NUMBER: 60/173,383

PRIOR APPLICATION NUMBER: 60/175,693

PRIOR APPLICATION NUMBER: 60/175,693

PRIOR APPLICATION NUMBER: 60/176,693

PRIOR FILING DATE: 12000-01-12

PRIOR FILING DATE: 2000-01-12

PRIOR FILING DATE: 2000-03-23

JUMPER OF SCO ID NOSA 43008
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US-11-097-143-12000
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                                                                                                                              NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FRANKSEQ for Windows
SEQ ID NO 12000
LENGTH: 364
            Query Match
Best Local Similarity
Matches 258; Conserv
                                                                                  -11-097-143-12000
                                                                                              ORGANISM:
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              Conservative
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                            70.1%; Score 1384; DB 6; 70.3%; Pred. No. 9.4e-121;
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                 51;
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il; Mismatches 54;
                 Mismatches
                                                Length 364;
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; ORGANISM: Anopheles
US-10-094-240-25
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US-10-094-240-25
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APPLICANT: ZWIEBEL, LAURENCE J.

TITLE OF INVENTION: ARRESTIN GENE, POLYPEPTIDE, AND METHODS OF USE THEREOF FILE REFERENCE: N8289

CURRENT APPLICATION NUMBER: US/10/094,240

CURRENT FILING DATE: 2001-03-08

PRIOR APPLICATION NUMBER: 10/056,405

PRIOR APPLICATION NUMBER: 60/264,649

PRIOR FILING DATE: 2001-01-26

PRIOR FILING DATE: 2001-01-26

NUMBER OF SEQ ID NOS: 27

SOCTWARE: PATENTIN VEY. 2.1

SEQ ID NO 25

LENGTH: 398
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                                                                                                                                                                                                                                                                                                                              Best Local Similarity Matches 204; Conserv
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                                                                                                                     SMAPSSVTLOAGEDDTGKPLGVEYAIKAHVGEDESDKGHKRSAVTLTIKKLQYAPVSRGR 178
                                                                                                                                                                                        YRYGREEDBYMGVKFSKEMVLTKEQIYPM-ENANMEMTPMQERLVKKLGANAFPFTFHFP 118
                                                     RLPSSLVSKGFTFSQGKINLEVTLDREIYYHGEKIAANIVVTNNSRKTVKSIKCFVVQHC
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Sequence 241, Application US/10954778
Publication No. US20050153368A1
GENERAL INFORMATION:
APPLICANT: ZWIEBEL, LAURENCE J.
TITLE OF INVENTION: METHOD OF IDENTIFYING CHE
TITLE OF INVENTION: ODDORANT RECEPTORS OF SEN
FILE REFERENCE: N1125
CURRENT FILING DATE: 2004-09-30
PRIOR APPLICATION NUMBER: US/10/954,778
CURRENT FILING DATE: 2002-01-24
PRIOR FILING DATE: 2002-01-24
PRIOR PELICATION NUMBER: 60/264,649
PRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 248
SOPTWARE: PATENTIN PATENTIN SEQ ID NO 241
LENGTH: 398
TYPE: PRT
             US-11-097-143-1314
; Sequence 1314, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
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US-10-954-778-241
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                                                                                         RESULT 8
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Best Local
   APPLICANT: Venter, J.
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Similarity 52.3%; Pred. No. 7.5e-87;
04; Conservative 65; Mismatches 111; Indels
                                                                                                                                                                                                                       VNLASSTLISEGKCPSDAMGIVISYSLRVKLNCGTLGGELQTDVPFKLMNPAPGSVERER
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                                                                                                                                                                                                                                                                                                                                                                    RLPSSLVSKGFTFSQGKINLEVTLDREIYYHGEKIAANIVVTNNSRKTVKSIKCFVVQHC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                            SMAPSSVTLOAGEDDTGKPLGVEYAIKAHVGEDESDKGHKRSAVTLTIKKLQYAPVSRGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YRYGREEDEVMGVKFSKEMVLTKEQIYPM-ENANMEMTPMQERLVKKLGANAFPFTFHFP 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EVTMV-NAQFSKHIASLETREGCPITPGASFTKSFFLVPLASSNKDRRGIALDGHLKEDD
                                                                                                                                                VNALKKMKSIERHRYENSHYADDDDNIVFE
                                                                                                                                                                                   VIHADSQADVETFRODT - - - IDQQASVDFE
                                                                                                                                                                                                                                                                                               EVTMV-NAQFSKHIASLETREGCPITPGASFTKSFFLVPLASSNKDRRGIALDGHLKEDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHEMICAL AGENTS
SENSORY NEURONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WHICH STIMULATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                            178
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                                                                                                                                              RESULT 9
US-10-094-240-27
; Sequence 27, Application US/10094240
; Publication No. US20030082637A1
; GENERAL INFORMATION:
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Best Local
APPLICANT: ZWIEBEL, LAURENCE J.
TITLE OF INVENTION: ARRESTIN GENE, POLYPEPTIDE, AND METHODS OF USE THEREOF
FILE REFERENCE: N8289
CURRENT APPLICATION NUMBER: US/10/094,240
CURRENT FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: 10/056,405
PRIOR APPLICATION NUMBER: 10/056,405
PRIOR APPLICATION NUMBER: 60/264,649
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TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,0
TITLE OF INVENTION: DROSOPHILA GENES.
FILE REFERENCE: CL000728
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: 60/157,83
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-09
PRIOR APPLICATION NUMBER: 60/161,93
PRIOR FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: 60/173,693
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR FILING DATE: 1990-10-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version SEQ ID NO 1314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/184,831
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60/191,637
PRIOR FILING DATE: 2000-03-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                286 TAQYKSVVAEIESEDGCQVAPGFTLSKVFELCPLLANNKDKWGLALDGQLKHEDTNLASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 KVFKKCAPNGKVTLYMGKRDFVDHVSGVEPIDGIVVLDDEYIRDNRKVFGQIVCSFRYGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            470
                      TLLAQPDQRDAFGVIISYAVKVKLFLGA--LGGELSAELPFVLMHPKF 351
                                                                                                                                            NGSYRNTVASLETSEGCPIQPGSSLQKVMYLTPLLSSNKQRRGIALDGQIKRQDQCLAST 305
                                                                                                                                                                                                                                       VRKDFMLSPGELELEVTLDKQLYLHGERIGVNICIRNNSNKMVKKIKAMVQQGVDVVLFQ
                                                                                                                                                                                                                                                                                                               BEDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKKLGSNAIPFTFNISPNAPS
TLITNPAQRESLGIMVHYKVKVKLLISSPLLNGDLVAELPFTLMHPKP
                                                                                                                                                                                                            VSKEFMMKPNKIHLEATLDKELYHHGEKISVNVHVANNSNRTVKKIKVCVRQFADICLFS
                                                                                                                                                                                                                                                                                                                                                              SVILQQGEDDNGDPCGVSYYVKIFAGESETDRTHRRSTVTLGIRKIQFAPTKQGQQPCTL 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RVFKKSSSNGKITVYLGKRDFVDHVTHVDPIDGVVFIDPEYVKD-RKVFGQVLAAFRYGR
                                                                                                                                                                                                                                                                                                                                                                                                                        EDLDVLGLTFRKDLYLAHEQIYP-PMQLDRPMTRLQERLIKKLGPNAHPFYFEVPPYCPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.8%; pred. No. ...
/ 53.7%; pred. No. ...
--ive 70; Mismatches
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Pred. No. 9e-85;
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; SOFTWARE: PatentIn Ver.
; SEQ ID NO 27
; LENGTH: 401
; TYPE; PRT
; ORGANISM: Drosophila m
US-10-094-240-27
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                                 PRIOR APPLICATION NUMBER: 60/157,832
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR APPLICATION NUMBER: 60/184,831
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60/184,837
PRIOR FILING DATE: 2000-03-23
PRIOR FILING DATE: 2000-03-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12684, Application US/11097143
Publication No. US20050208558A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Venter, J. Craig
APPLICANT: et al.
APPLICANT: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS
TITLE OF INVENTION: ARRAYS, FOR DETECTING
TITLE OF INVENTION: DROSOPHILA GENES.
FILE REFERENCE: CLOOO728
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT FILING DATE: 2005-04-04
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NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSEQ
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               FILING DATE: 2000-02-24
APPLICATION UNMER: 60/191,637
FILING DATE: 2000-03-23
R OF SEQ ID NOS: 43008
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MYYNFKVFKKCAPNGKVTLYMGKRDFVDHVSGVEPIDGIVVLDDEYIRDNRKVFGQIVCS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRYGREEDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKKLGSNAIPFTFNIS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MVVSVKVFKKATPNGKVTFYLGRRDFIDHIDYCDFVDGVIVVEPDYLK-NRKVFGQLATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DVVLFQNGSYRNTVASLETSEGCPIQPGSSLQKVMYLTPLLSSNKQRRGIALDGQIKRQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---KAKVIHADSQADVETFRODTIDQQASVDF 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QCLASTTLLAQ-PDQRDAFGVIISYAVKVKLFLGALGGELSAELPFVLMHPKPGT-----
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; Pred. No. 4.8e-83;
73; Mismatches 115;
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EXPRESSION OF 10,000
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; SEQ ID NO 12684
; LENGTH: 401
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-12684
                                                                                                                                                                                                                                    ; LENGTH: 410
; TYPE: PRT
; ORGANISM: Homo s
US-09-880-137-3
                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Berstein, Gabriel
APPLICANT: Berstein, WETHODS OF ASSAYING FOR
ITITLE OF INVENTION: PROTEIN-COUPLED RECEPTC
FILE REFERENCE: MNI-131
CURRENT APPLICATION NUMBER: US/09/880,137
CURRENT FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: US 60/186,706
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
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US-09-880-137-3
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Best Local :
                                                                                                                                                                                                                                                                                                        SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/09880137 Patent No. US20020031295A1
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                                                                                                                                                                       Matches
                                                                                                                                                                                                     Query Match
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Local Similarity 48.7%; Pi
1es 191; Conservative 73;
                                                                                                                                                                       Local Similarity
les 176; Conserv
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                                                                                                 ---KAKVIHADSQADVETFRQDTIDQQASVDF
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                                  EDLDVLGLTFRKDLFVANVQSFPPAPEDKKPLTRLQERLIKKLGEHAYPFTFEIPPNLPC
                                                                  EEDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKKLGSNAIPFTFNISPNAPS 125
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Pred. No. 4.8e-83;
                                                                                                                                                                       Score 907.5; DB 3;
Pred. No. 5.3e-76;
8; Mismatches 112;
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RESULT 12
US-09-800-137A-3
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; ORGANISM: Homo sapiens
US-09-800-137A-3
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PRIOR TILING DATE: 2001-03-05
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FASUSEQ for Windows Version 4.0
SEQ ID NO 3
SEQ ID NO 3
LENGTH: 410
TYPPE: Nor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 46.0%; Score 907.5; DB 3; Best Local Similarity 47.2%; Pred. No. 5.3e-76; Matches 176; Conservative 78; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: MNI-131
CURRENT APPLICATION NUMBER: US/09/800,137A
CURRENT FILING DATE: 2001-03-05
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TITLE OF INVENTION: METHODS OF ASSAYING FOR G
TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
363
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                              QADVETFRODTID 375
                                                                                TLLAQPDQRDAFGVIISYAVKVKLFLGALGGELSAELPFVLMHPKPGTK---AKVIHADS 362
                                                                                                                                    TAQYKCPVAMEEADD -- TVAPSSTFCKVYTLTPFLANNREKRGLALDGKLKHEDTNLASS
                                                                                                                                                                  NGSYRNTVASLETSEGCPIQPGSSLQKVMYLTPLLSSNKQRRGIALDGQIKRQDQCLAST 305
                                                                                                                                                                                                      TTROFLMSDKPLHLEASLDKEIYYHGEPISVNVHVTNNTNKTVKKIKISVRQYADICLFN
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Sequence 1, Application US/09800137A
Publication No. US20030157553A1
GENERAL INFORMATION:
APPLICANT: Berstein, Gabriel
TITLE OF INVENTION: METHODS OF ASSAVING FOR G
TITLE OF INVENTION: MOTHODS OF ASSAVING FOR G
TITLE REFERENCE: MNI-131
CURRENT FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: US/09/800,137A
CURRENT FILING DATE: 2001-03-05
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 418
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US-09-880-137-1
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CURRENT FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: US 60/186,706
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
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Patent No. US20020031295A1
GENERAL INFORMATION:
APPLICANT: Berstein, Gabriel
TITLE OF INVENTION: METHODS OF ASSAYING FOR G
TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
FILE REFERENCE: NNI-131
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Best Local Similarity
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TYPE: PRT
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RESULT 15
US-10-038-010-52
; Sequence 52, Application US/10038010
; Publication No. US20030040089A1
; GENERAL INFORMATION:
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 밁
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TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: beta Arrestin 1
LOCATION: (1)..(452)
OTHER INFORMATION:
IS-10-038-010-52
                                                                                                                 Query Match
Best Local S
Matches 179
                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/038,010
CURRENT FILING DATE: 2002-07-23
PRIOR APPLICATION NUMBER: US 60/259,377
PRIOR FILING DATE: 2001-01-02
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin version 3.1
SEQ ID NO 52
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APPLICANT: Pierre, Legrain
TITLE OF INVENTION: Protein-protein interactions in adipocyte
FILE REFERENCE: B4767A
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                EEDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKKLGSNAIPFTFNISPNAPS 125
                                                                                                               45.8%; Score 903.5; DB 4; llarity 47.1%; Pred. No. 1.5e-75; Conservative 76; Mismatches 112;
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EVPEHETPVDTNLIELDTND 383
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Search completed: May 20, 2006, 23:06:38
Job time: 182 secs

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Minimum
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| Memc Celerra SIDS3/ptcdata/2/pubpaa/US06_NEW PUB.pep:*
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US-10-316-312-255-928-315
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202, Appl

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310, Appl

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Sequence 173, Application US/10505928

Publication No. US20060088532A1

GENERAL INFORMATION:
APPLICANT: Ludwig Institute for Cancer Research et TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
FILE REFERENCE: 28967/39178

CURRENT APPLICATION NUMBER: US/10/505,928

CURRENT FILING DATE: 2004-08-27

PRIOR APPLICATION NUMBER: US 60/363,019

PRIOR APPLICATION NUMBER: US 60/363,019

PRIOR FILING DATE: 2002-03-07

NUMBER OF SEG ID NOS: 866

SOFTWARE: Patentin 3.2

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TYPE: PRT
ORGANISM: Homo sapiens
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US-11-280-757-35	US-11-183-218-30		US-10-511-937-2597	US-11-183-218-66	-10-505	US-10-478-743B-4	US-11-249-111-123	US-10-505-928-357	US-10-511-937-2463	US-11-170-482-18	US-10-322-836-50	US-10-511-937-2545	US-10-505-928-75	US-11-251-465-31	US-10-505-928-363	US-11-327-900-8	US-10-505-928-513	US-11-311-778-20	US-10-370-959-135
Sequence 35,	Sequence 30,	æ	O	æ	Sequence 259,		Sequence 123	Sequence 357,	Sequence 246	Sequence 18,	Sequence 50,	Sequence 254		Sequence 31,	Sequence 363,	Sequence 8, 1	- 1	Sequence 20,	
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                                                               NGSYRNTVASLETSEGCPIQPGSSLQKVMYLTPLLSSNKQRRGIALDGQIKRQDQCLAST 305
                                                                                                   TTRHFLMSDRSLHLEASLDKELYYHGEPLNVNVHVTNNSTKTVKKIKVSVRQYADICLFS
                                                                                                                  SVTLQQGEDDNGDPCGVSYYVKIFAGESETDRTHRRSTVTLGIRKIQFAPTKQGQQPCTL
TAQYKCPVAQLEQDD--QVSPSSTFCKVYTITPLLSDNREKRGLALDGKLKHEDTNLASS
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US-10-511-937-2974

RESULT 2

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PRIOR APPLICATION NUMBER: PCT/US2003/012946
PRIOR FILING DATE: 2003-04-24
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: US 10/325,899
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: Patentin version 3.2
SEQ ID NO 2974
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US-10-511-937-2974
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APPLICANT: EXPRESSION DIAGNOSTICS,
APPLICANT: Wohlgemuth, Jay
APPLICANT: Fry, Kirk
                                                                                                                                                                                                                                Sequence 478, Application US/10196749 Publication No. US20060094864A1
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CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT FILING DATE: 2004-10-19
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APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
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                                                                                                                                                                                       Baker, Kevin P.
                                                                                                                                                                                                                                                                                                                                                         RKNGFDFVIDENAPVTERAKLISLPTSKNWTFGP----QDVDELIFMLSDS
                                                                                                                                                                                                                                                                                                                                                                                                                                         VDQHATDEKYNFEM-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FKKEEILSSSDICQKLVNT-QDMSASQVDVAVKINKKVVPLDFSMSSLAKRIKQLHHEAQ 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FQKELCLASEQIYPRPEKSDKEQTKLQERLLKKLGSNAIPFTFNISPNAPSSVTL-QQGE 133
Smith, Victoria Watanabe, Colin E Wood, William I.
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                                                                                    Gurney, Austin L.
                                                                                                     Goddard, Audrey
Godowski, Paul
                                                                                                                                                Desnoyers, Luc
                                                                Pan, James
                                                                                                                                                                      Chen, Jian
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; TYPE: PRT ; ORGANISM: Homo Sapien US-10-196-749-478
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CURRENT FILING DATE: 2002-07-16
PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR APPLICATION NUMBER: 60/059263
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/063120
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-10-24
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/063121
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063486
PRIOR FILING DATE: 1997-10-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 1997-10-28
APPLICATION NUMBER: 60/063544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/063540 FILING DATE: 1997-10-28
                                                                                                                                                                                                                                                                                           310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       205
472 SVSATDRDSGTNAQVTYSLLPPQDPHLPLASLVSINADNG---HLFALRSLDYEALQAFE 528
                                                                                                                                              294 QIKRQDQCLASTTLLAQPDQRDAFGVII------SYAVKVK------LFLG 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54 FGQIVCSFRYGREEDEVMGLN------FQKELCLASE-QIYPR---PEKSDKEQ 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QGELSTTTTALDGGSPSRSGTSTVRIVVLDVNDNAPQFAQALYETQAPENSPIGF-LIVK
                                                  ALGGE-----LSAELPFVLMHPK----PGTKAKVIHADSQADVETFRQDTIDQQASVDFE 383
                                                                                               EIRAEYNITITVTDLGTPRLKTEHNITVLVSDVNDNAPAFTQTSYTLFVRENNSPALHIG
                                                                                                                                                                                           NSVA--ENSPETPLAVFKINDRDSGENGKMVCYIQENLPFLLKPSVENFYILITEGALDR 411
                                                                                                                                                                                                                                           NTVASLETSEGCPI-----QPGSSLQKVMYLTP----LLSSNKQRRGI-----ALDG 293
                                                                                                                                                                                                                                                                                             ELV------NSYKI--NİQAMDGGĞLSARCRVLVEVLDTNDNPPELIVSSFS 353
                                                                                                                                                                                                                                                                                                                                                                                                                                  IFAGESETDRTHRRSTVTLGIRKIQFAPTKQGQQPCTLVRKDFMLSP--GELELEVTLDK 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----AFRLERAQDPDGGLNGIQNYTISPNSFFHINISGGDEGMIYPELVLDKALDREE
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                                                                                                                                                                                                                                                                                                                                     QLYLHGERIGVNICIRNNSNKMVKKIKAMVQQGVDV-----VLFQN------GSYR 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         263
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RESULT 4 US-10-505-928-201

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Sequence 201, Application US/10505928
Publication No. US2006008532A1
GENERAL INFORMATION:
APPLICANT: Ludwig Institute for Cancer Research et al.
TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
FILE REFERENCE: 28967/39178
CURRENT APPLICATION NUMBER: US/10/505,928
CURRENT FILING DATE: 2004-08-27
PRIOR APPLICATION NUMBER: US 60/363,019
PRIOR PILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 866
SOFTWARE: Patentin 3.2
SEQ ID NO 201
IENCTH. 1212
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US-11-251-466-46
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                                                              SEQ ID NO 46
LENGTH: 282
TYPE: PRT
ORGANISM: Yarrowia lipolytica
S-11-251-466-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 46, Application US/11251466 Publication No. US20060094090A1
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Query Match
Best Local Similarity
                                                                                                                                                                    FILE REFERENCE: CL2793 USNA CURRENT APPLICATION NUMBER: US/11/251,466 CURRENT FILING DATE: 2005-10-14 PRIOR APPLICATION NUMBER: US 60/624812 PRIOR FILING DATE: 2004-11-04 NUMBER OF SEQ ID NOS: 55 SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                                                 APPLICANT: Xue, Zhixiong
APPLICANT: Damude, Howard Glenn
APPLICANT: Damude, Howard Glenn
TITLE OF INVENTION: A MORTIERELLA ALPINA LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE
TITLE OF INVENTION: HOMOLOG FOR ALTERATION OF POLYUNSATURATED FATTY ACIDS AND OIL
TITLE OF INVENTION: CONTENT IN OLEAGINOUS ORGANISMS
                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: E.I. duPont de Nemours and Company
APPLICANT: Xue, Zhixiong
APPLICANT: Damude, Howard Glenn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1212
TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   568 PSSRPSSVYGLDLSİKRDSSSSSLRLKAQEAEALDV-----SFSHASSSARTKPTSLPİ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56 QIVCSFRYGREE-DEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKKLGSNAIP 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VTLGIRK----IQFAPTKQGQQPCTL---VRKDFMLSPGELELEVTLDKQLYLHGER--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FTFN-----ISPNAPSSVTLQQGEDDNGDPCGVSYYV----KIFAGESETDRTHRRST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AVKVKLFLGALGGELSAELPFVLMHPKPGTKAKVIHADSQADVETFRQDTIDQQA 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SQSRG-----RIPIVAQNSEEESPLSPVGQPMGMARAAAGPLPPISADTRDQFG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QPGSSLQKVMYLTPLLSSNKQRRG-IALDGQIKRQDQCLASTTLLAQPDQRDAFGVIISY
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3.9%;
  Score
Pred.
    77;
No.
    0.49;
                        DB 7;
                        Length
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RESULT 6
US-11-264-784-72
; Sequence 72, Application US/11264784
; Publication No. US20060094092A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                            Query Match
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APPLICANT:
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CURRENT APPLICATION NUMBER: US/11/264,784
CURRENT FILING DATE: 2005-11-01
NUMBER OF SEQ ID NOS: 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: E.I. duPont de Nemours & Co., APPLICANT: Damude, Howard Glenn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 282
                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          194 PGELEL-----EVTLDKQLY---LHGERIGVNICI---RNNSNKMVKKIKAMVQ 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144 YYVKIFAGESETDRTHRRSTVTLGI--RKIQFAP-----TKQGQQPCTLVRKDFMLS 193
                                284
222
                                                                                                                                                                                                                                         144 YYVKIFAGESETDRTHRRSTVTLGI--RKIQFAP-----TKQGQQQPCTLVRKDFMLS 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              222 TSRMFSFGRGKLDAGEILVDVLSPIETKGLDASNVDALMATTYKAMCETADQIG
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                                                                                                                                                                                                                                                                             58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIQSGNGGKGQSVFMFPEGTRSYSKDVGIMPFKKGCFHLAVQSGAP-----IVPVVVQN 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----QGVDVVLFQNG--SYRNTVASLETSEGC---PIQPGSSLQKVMYLTPLLSSN 283
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TSRMFSFGRGKLDAGEILVDVLSPIETKGLDASNVDALMATTYKAMCETADQIG 275
                                                                                                                                   QNEMDILVLGRIFPQYCSVTAKKALKWYPLLGQFMALSGTIFLDRKDRTKSVQTLGGAVK
                                                                                                                                                                     PGELEL-----RINSNKMVKKIKAMVQ
                                                                                                                                                                                                      YSVRIFLGISIKLRS-ROVTGTAGLDASKIQVANTTKPIDDITKHLPRPCILISN----H 107
                                KQR----RGIALDGQI---
                                                                 TIQSGNGGKGQSVFMFPEGTRSYSKDVGIMPFKKGCFHLAVQSGAP-----IVPVVVQN
                                                                                                -----QGVDVVLFQNG--SYRNTVASLETSEGC---PIQPGSSLQKVMYLTPLLSSN
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Macool, Daniel Joseph
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Zhang, Hongxiang
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                                                                                                                                                                                                                                                                                              Score 77; DB 7
Pred. No. 0.49;
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                                                                                                                                                                                                                                                                               Mismatches
                                -KROD----OCLASTTLLAQPDQRDAFG 318
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US-10-505-928-733, Application US/10505928; Sequence 733, Application US/10505928; Publication No. US2006008853ZA1; GENERAL INFORMATION:

RESULT 7

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SEQ ID NO 733
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CURRENT APPLICATION NUMBER: US/10/505,928
CURRENT FILING DATE: 2004-08-27
PRIOR APPLICATION NUMBER: US 60/363,019
PRIOR APPLICATION STATE OF SEQ ID NOS: 866
     APPLICANT:
TITLE OF II
                                                                                                                                                                  APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian APPLICANT: Desnoyers, Luc
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TYPE: PRT
ORGANISM: Homo sapiens
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T: Zhang, Zemin
INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
                                    Pan, James
Smith, Victoria
Watanabe, Colin K.
Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                               QDT 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IISYAVKVKLFLGALGGELSAELPFV--
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                                                                                                               Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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Sequence 16, Application US/11170482
Diblication No. US20060094037A1
GENERAL INFORMATION:
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; ORGANISM: mouse US-11-170-482-16
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PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120
PRIOR APPLICATION NUMBER: 60/063121
PRIOR APPLICATION NUMBER: 60/063121
PRIOR APPLICATION NUMBER: 60/063121
PRIOR FILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-10-24
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SEQ ID NO 164
                                                                    SEQ ID NO 16
LENGTH: 708
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Best Local Similarity 26.2%; Pred. No. 1;
Matches 32; Conservative 21; Mismatches
                                                                                                                                                               FILE REFERENCE: 1034/1H570
CURRENT APPLICATION NUMBER: US/11/170,482
CURRENT FILING DATE: 2005-06-28
PRIOR APPLICATION NUMBER: US/09/945,258
PRIOR FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/229,889
PRIOR APPLICATION NUMBER: US 60/229,889
PRIOR APPLICATION NUMBER: US 60/229,889
PRIOR PILING DATE: 2000-09-01
                                                                                                                                                                                                                                                                                                                                      APPLICANT: Fraser, Paul E.
APPLICANT: University of Toronto
TITLE OF INVENTION: PROTEINS RELATED TO SCHIZOPHRENIA AND USES THEREOF
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                                                                                                                    NUMBER OF SEQ ID NOS: 19 SOFTWARE: FastSEQ for Windows Version 3.0
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PRIOR TILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063541
PRIOR FILING DATE: 1997-10-28
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                                             LENGTH: 70
TYPE: PRT
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PRIOR FILING DATE: 2004-08-27
PRIOR FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 866
SOFTWARE: Patentin 3.2
SEQ ID NO 304
LENGTH.
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US-10-505-928-304
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Best Local Similarity
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Best Local Similarity
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CURRENT FILING DATE: 2004-08-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ludwig Institute for Cancer Research et al. TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES FILE REFERENCE: 28967/39178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
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                                               GIALDGOIKRODOCLASTTLLAQPDORDAFG--VIISYAV----KVKLFLGALGGELSAE 341
                                                                                                                   VKKIKAMVQQGVDVVLFQNGSYRNTVASLETSEGCPIQPGSSLQKVMYLTPLLSSNKQRR 287
                                                                                                                                                       ---ETLGPKPAA---RDVNLPRPPGALCEQKRETCAD-----GEAAG---CTINNSLSN 183
                                                                                                                                                                                      FAPTKQGQQPCTLVRKDFML--SPG---ELELEVTLDKQLYLHGERIGVNICIRNNSNKM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/10505928 o. US20060088532A1
                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                QVKVEEPSRPSASWQNSVSERPPYSYMAMIQFAINSTERKRMTLKDIYTWIEDH
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                                                                                                                                                                                                                                                                                                                                                               t; Score 73; DB 6; Length 763
t; Pred. No. 7.4;
46; Mismatches 120; Indels
                                                                                    -GS-RSIKQEMEEKENCHLE---
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Pred. No. 4.4;
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                                                                                                                                                                                                                                                                                                                                                                                                   DB 6; Length 763;
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US-11-251-465-22
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RESULT 12
US-10-322-836-48
(Sequence 48, Application US/10322836
; Publication No. US20060090212A1
; GENERAL INFORMATION:
; APPLICANT: Turner, Alexander C., Jr
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Publication No. US20060094061A1
GENERAL INFORMATION:
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Best Local
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FILE REFERENCE = 930,172-A USA
CURRENT APPLICATION NUMBER: US/11/251,465
CURRENT FILING DATE: 2005-10-14
PRIOR APPLICATION NUMBER: 60/619,384
PRIOR PILING DATE: 2004-10-15
NUMBER OF SEQ ID NOS: 880
NUMBER OF SEQ ID NOS: 880
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
les 81; Conserv
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                                                                                                                                                                                                            VVLPAEEELVEADEAGSVYAGILSYGVGFFLFILVVA---AVTLCRLRSPPKKGLGSPTV
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                                                                                                                                           HKISRFPLK--RQVSLESNASM
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18.3%;
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WIMMBER OF SEQ ID NOS: 866
SOFTWARE: PatentIn 3.2
SEQ ID NO 310
LENGTH: 2215
TYPE: PRT
OCGANISM: Homo sapiens
US-10-505-928-310
                                                                                                                                                                                                                                                                                                                                                       US-10-505-928-310
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APPLICANT: Freidrich, Glenn A.
APPLICANT: Freidrich, Glenn A.
APPLICANT: Sands, Arthur T.
APPLICANT: Sands, Arthur T.
APPLICANT: Sonds, Arthur T.
APPLICATION: NOVEL HUMAN GENES AND PROTEINS
TITLE OF INVENTION: ENCODED THEREBY
FILE REFERENCE: 8535-0037-999
CURRENT APPLICATION NUMBER: US/10/322,836
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: US/09/579,114
PRIOR APPLICATION NUMBER: US/09/579,114
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 3.0
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; LOCATION: (179)...(179)
; OTHER INFORMATION: Xaa = Ser or
US-10-322-836-48
                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
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LENGTH: 1075
TYPE: PRT
                                                                                                                                                                                                                                                                                           Sequence 310, Application US/10505928
Publication No. US20060088532A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 3.7%;
Best Local Similarity 16.8%;
Matches 48; Conservative 4
Query Match
                                                                                                                                                        CURRENT FILING DATE: 2004-08-27
PRIOR APPLICATION NUMBER: US 60/363,019
PRIOR FILING DATE: 2002-03-07
NIMBER OF THE PRIOR FILING DATE: 2002-03-07
                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/505,928
CURRENT FILING DATE: 2004-08-27
                                                                                                                                                                                                                                     APPLICANT: Ludwig Institute for Cancer Research TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES FILE REFERENCE: 28967/39178
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LOCATION: (130)...(130)
OTHER INFORMATION: Xaa =
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 234 MV-----QQGVDVV-----LFQNGSYRNTVASLETSEGCP 263
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3.7%;
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Pred. No. 15;
48; Mismatches
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Score 72.5;
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Length 2215;
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) ORGANISM: Homo sapiens US-10-511-937-2451
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CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: PCT/US2003/012946
PRIOR FILING DATE: 2003-04-24
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR FILING DATE: 2002-04-24
PRIOR PRIOR DATE: 2002-04-24
PRIOR APPLICATION NUMBER: US 10/325,899
PRIOR FILING DATE: 2002-12-20
PRIOR FILING DATE: 2002-12-20
                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 3117
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2451
LENGTH: 798
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Ly, Ngoc
APPLICANT: Prentice, James
APPLICANT: Morris, MacDonald
APPLICANT: Morris, MacDonald
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: EXPRESSION DIAGNOSTICS, APPLICANT: Wohlgemuth, Jay
                                                                                                                                                                                  Local Similarity
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107 -----KLGSNAIPFTFNISPNAPSSVTLQQGEDDNG---
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                                                            QDSESVWSDIECAALVGEDQ------PLC-----PDLPELDLSELDVNDLDT
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Sequence 1, Application US/11316132

Publication No. US20060100153A1

GENERAL INFORMATION:
APPLICANT: Shridhar, Viji
APPLICANT: Roberts, Lewis R.
APPLICANT: Kaufmann, Scott H.
TITLE OF INVENTION: HSulf-1 Nucleic Acids, Polypeptides and TITLE OF INVENTION: HSulf-1 Nucleic Acids, Polypeptides and TITLE OF INVENTION: Wethods of Using
FILE REFERENCE: 07039/449001

CURRENT FILING DATE: 2005-12-22

PRIOR APPLICATION NUMBER: US/11/316,132

CURRENT FILING DATE: 2005-12-22

PRIOR FILING DATE: 2004-02-12

PRIOR APPLICATION NUMBER: US/10/778,607

PRIOR APPLICATION NUMBER: 60/446,945

PRIOR FILING DATE: 2003-02-12

NUMBER OF SEQ ID NOS: 41

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1

LENGTH: 871

TYPE: PRT

ORGANISM: Homo sapiens
Search completed: May 20, 2006, 23:06:54 Job time : 12 secs
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                                                                                                               668 ---KRRKPEE------CSCSKQSYYNKEKGVKKQEKLKSHL 699
                                                                                                                                            60 SFRYGREEDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERL 104
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SUMMARIES

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Aag67783 Amino aci	Yello		Adr23187 Yellow fl	Aef35191 Beta-arre	Aef35190 Beta-gala	Ade58181 Rat Prote	Ade58177 Rat Prote	Abg69496 Rat bait	PRO	Adn95251 Human BEC	Ade58179 Human Pro	Ade58183 Human Pro	Aag67781 Amino aci	Aag67784 An exempl			Aag67785 An exempl		Abb61736 Drosophil	Abr84476 Mosquito	ophel	Description	•

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ALIGNMENTS

RESULT 1
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X Anopheles gambiae; mosquito; olfactory gene; arrestin 1; pest control; odourant receptor; olfaction. 01-NOV-2002 ABP52833; Zwiebel LJ, 26-JAN-2001; 2001US-0264649P. 24-JAN-2002; 2002US-00056405. 28-JAN-2002; 2002WO-US002549 01-AUG-2002. WO200259274-A2. Anopheles gambiae. Anopheles gambiae arrestin 1 protein SEQ ID NO:2. ABP52833 standard; protein; (UYVA-) UNIV VANDERBILT. (first entry) 383

New mosquito olfaction polypeptides and polynucleotides, useful for mosquito management, i.e. controlling the pest and disease vectors, for identifying pest control agents. or

WPI; 2002-627421/67. N-PSDB; ABQ75102.

Claim 18; Fig 2; 96pp; English.

The present invention describes a purified Anopheles gambiae olfaction polypeptide comprising a 383, 394, 380, 411, 412, 391, 157 or 401 residue amino acid sequence (see ABP52833 to ABP52840) (S1), a conservatively modified amino acid sequence of them, or a sequence of (S1) with at least 20 consecutive residues. Also described: (1) an isolated polynucleotide comprising: (a) a nucleotide sequence encoding the purified Anopheles gambiae olfaction polypeptide; or (b) a nucleotide sequence that hybridises under stringent conditions to a hybridisation probe comprising a 1964, 1239, 1142, 1236, 1194, 1176, 474 or 1206 nucleotide sequence

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RESULT 2
ABR84476
ID ABR8
XX
AC ABR8
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DT 15-J
XX
MOSQ
XX
MOSQ
XX
ANOE
XX
ANOE
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PN WO2C
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                                             08-MAR-2002; 2002US-00094240
                                                                             10-MAR-2003;
                                                                                                            18-SEP-2003
                                                                                                                                         WO2003076590-A2
                                                                                                                                                                                                      Arrestin 1;
                                                                                                                                                                                                                                     Mosquito olfaction molecule, arrestin 1.
                                                                                                                                                                                                                                                                      15-JAN-2004
                                                                                                                                                                                                                                                                                                                                   ABR84476 standard; protein;
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                  (UYVA-) UNIV VANDERBILT
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                                                                                                                                                                       gambiae
                                                                                                                                                                                                      mosquito;
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RESULT 3
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Best Local
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                  pharmaceutical
                                Drosophila; developmental biology; cell signalling; insecticide;
                                                                   Drosophila melanogaster polypeptide SEQ ID NO 12000
                                                                                                       26-MAR-2002
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DB; ACF79716.
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ilarity 100.0%;
Conservative 0
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Pred. No. 0;
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RESULT 4
ADQ89588
ID ADQ8
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ADQ89588
XX
AC ADQ8
XX
AC ADQ8
XX
Anta
XX
Cytc
KW Celi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL01676-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                 10-JAN-2003; 2003US-0439123P
06-MAY-2003; 2003US-0468402P
                                                                                     31-DEC-2003; 2003WO-GB005635
                                                                                                                                      WO2004063362-A2
                                                                                                                                                             Drosophila melanogaster
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genes from Drosophila and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arrestin; phosphorylation-independent arrestin mutant; grotein-coupled receptor; GPCR; GPCR ligand; pretinitis pigm stationary night blindness; colour blindness; nephrogenic DI; isolated glucocorticoid deficiency; hyperfunctioning thyroid familial hypocalciuric hypercalcemia; hyperparathyroidism;
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N-PSDB; ADQ89587.
                                                                                     Identifying a G protein-coupled receptor ligand, useful for treating retinitis pigmentosa, color blindness or neurlogical disorders, uses phosphorylation-independent arrestin mutants particularly suited for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unidentified.
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Disclosure; Page 47; 47pp; English

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N-PSDB;
The present sequence is the protein sequence of arrestin 2, a novel mosquito olfaction molecule. The invention provides 9 novel mosquito
                                                                                                           Claim 16; Fig 12b; 101pp; English.
                                                                                                                                                                                   New mosquito arrestin 1 and 2 genes and polypeptides, useful identifying mosquito olfaction molecule binding compounds whithe ability of mosquitoes to locate sources of bloodmeal, e.c
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zwiebel
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DB; ACF79731.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mosquito;
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                                                                                                                                                                               g compounds which reduce bloodmeal, e.g. humans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polypeptides and the nucleic acids encoding them. These are arrestins 1 and 2 and odorant receptor molecules 1-7. The odorant receptors function in a ligand-induced signal transduction pathway for the activation of mosquito olfaction. Arrestin functions to inhibit the activated signal transduction cascade. Thus, the odorant receptors act as an 'on' switch, and arrestin as an 'off' switch for the odorant detection system of the mosquito. Methods are provided for identifying compounds that interfere with the operation of the mosquito olfactory system, particularly compounds that modulate arrestin 2 activity. These are useful for the control of mosquitoes, particularly by reducing their ability to locate sources of bloodmeal
                                          The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventior useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly that the patent did not format directly are the control of the sequences.
                                                                                                                                                                                                                                                               New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                               23-MAR-2000;
11-JUL-2000;
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DB; ABL06067.
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                                at ftp.wipo.int/pub/published_pct_sequences
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2000US-00614150
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                                                                                                                                                                                                                                                                 detection reagent for detecting 1000 or more for elucidating cell signaling and cell-cell
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                                                                       The present sequence represents an exemplary phosphorylation-independent cc arrestin mutant. Such mutants are used in screening assays to identify cliptands and/or modulators of G protein-coupled receptors (GPCRs). A cc method for identifying a GPCR ligand comprises contacting a composition cc comprising the GPCR and a constitutively active arrestin mutant with a cc test compound; and determining the ability of the test compound to comodulate binding of arrestin mutant to the GPCR, where modulation of cc binding indicates that the test compound is a GPCR ligand. The method is cused for identifying potential ligands and/or modulators of GPCRs, coparticularly modulators, for use as human therapeutics. Modulators of GPCR may be used for treating patients having e.g. retinitis pigmentosa, cc stationary night blindness, colour blindness, nephrogenic DI, isolated contaction hypercalcemia, hyperfunctioning thyroid adenomas, familial cc disorders. The methods may be used for screening pluralities of test compounds (e.g. a small molecule library of compounds) or a composition containing a plurality of GPCRs. The methods may be used in screening cc assays for identification of natural and surrogate agonists of orphan cc GPCRs, and for identification of GPCR antagonists and/or agonists
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Best Local :
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 47; 47pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying a G protein-coupled receptor ligand, useful for treating e.g. retinitis pigmentosa, color blindness or neurlogical disorders, uses phosphorylation-independent arrestin mutants particularly suited for in
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                                                 Sequence
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                                                      CC describes phosphorylation-independent arrestin mutants. These mutants are CC used in screening assays to identify ligands and/or modulators of G CC protein-coupled receptors (GPCRs). A method for identifying a GPCR ligand CC comprises contacting a composition comprising the GPCR and a CC constitutively active arrestin mutant with a test compound; and CC determining the ability of the test compound to modulate binding of CC determining the ability of the test compound to modulate binding of CC potential ligand and/or modulators of GPCR and a GPCR ligand. The method is used for identifying CC potential ligands and/or modulators of GPCRs, particularly modulators, CC for use as human therapeutics. Modulators of GPCR particularly modulators, CC for use as human therapeutics. Modulators of GPCR any be used for treating patients having e.g. retinitis pigmentosa, stationary night CD bindness, colour bindness, nephrogenic DI, isolated glucocorticoid deficiency, hyperfunctioning thyroid adenomes, familial hypocalciuric CC hypercalcemia, hyperparathyroidism and neurological disorders. The methods may be used in screening assays for CC small molecule library of compounds) or a composition containing a CC small molecule library of compounds) or a composition containing a CC identification of natural and surrogate agonists of orphan GPCRs, and for identification of GPCR antagonists and/or agonists
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 46; 47pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying a G protein-coupled receptor ligand, useful for treating retinitis pigmentosa, color blindness or neurlogical disorders, uses phosphorylation-independent arrestin mutants particularly suited for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-MAR-2000; 2000US-0186706P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents an arrestin protein. The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               screening assays.
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Sequence 409 AA;

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RESULT
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Comprising the vector, a method for identifying a nucleotide a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a CC kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal CC subjected to pain, a method for identifying an agent CC expressed in an animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially CC expressed in an animal subjected to pain, a method for identifying a CC compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a CC method for identifying a compound or small molecula that regulates the CC specification, a method for identifying a compound useful in treating CC pain and a pharmaceutical composition comprising the one or more CC polypeptides or their antibodies. The polypucleotide given in the computates its activity is useful for preparing a medicament for treating CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction conjury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention discloses a composition comprising two or more isolat or human polynucleotides or a polynucleotide which represents a fra derivative or allelic variation of the nucleic acid sequence. Also
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GENBANK; P32121.
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01-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page; 1017pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
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(FARB )
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segmental nerve injury; chronic constriction injury; CCI;
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BAYER AG.
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0.13;
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CC or human polynucleotides or a polynucleotide which represents a fragment, CC derivative or allelic variation of the nucleic acid sequence. Also CC claimed are a vector comprising the nucleic acid sequence. Also CC claimed are a vector comprising the novel polynucleotide, a host cell CC comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a CC kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence CC that is differentially expressed in neuronal tissue of a first animal CC subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially CC expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the CC method for identifying a compound that regulates the activity in an animal of one or more of the polynucleotides, a method for identifying a compound useful in treating compound a pharmaceutical composition comprising the one or more of the polynucleotides or their antibodies. The polynucleotide or the compound that regulates the cc pain and a pharmaceutical composition comprising the one or more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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GENBANK; P32121.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            two or more isolated polypeptides, useful treating pain in an animal.
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                         This invention relates to a method of differentially modulating the growth or differentiation of blood endothelial cells (BEC) or lymphatic endothelial cells (LEC) comprises contacting endothelial cells with a composition comprising an agent that differentially modulates blood or lymphatic endothelial cells. Treating hereditary lymphoedema comprises identifying a human subject with lymphoedema and with a mutation in at least one allele of a gene encoding a LEC protein, where the mutation correlates with lymphoedema in human subjects, and with the proviso that the LEC protein is not VEGFR-J; and administering to the subject a composition comprising a lymphatic growth agent selected from VEGF-C or VEGF-D polypeptides and polynucleotides. The invention may be useful for the development of compounds with an antiangiogenic, cytostatic, vasotropic or antiinflammatory activity or for gene therapy. The method is useful in modulating the growth or differentiation of blood endothelial cells or lymphatic endothelial cells, in treating hereditary lymphoedema, in screening for an endothelial cell disorder or travicity or for gene therapy or travicity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-MAR-2002; 2002US-0363019P.
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0.13;
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                                                                polypeptide. The polypeptide, agonist or an antagonist, composition, and method are useful for diagnosing and treated disorder, e.g. systemic lupus erythematosus, rhe arthritis. The present sequence represents a DNA encoding
                                                                                                                                                                                                                                                        New nucleic acid encoding PRO polypeptide, useful for diagnosing and treating an immune related disorder, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antirheumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic; Antithyroid; Antidiabetic; Nephrotropic; CNS-Gen.; Hepatotropic; Virucide; Gastrointestinal-Gen.; Antipsoriatic; Antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRO polypeptide SEQ ID NO 874.
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                                                                                                                                                                                                                 Claim
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                                                                                                                                                                 The invention relates to an isolated nucleic acid encoding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           indexer using the source data given in table 14 of the specification
                                                                                                                                                                                                                                                                                                                                                          2005-182330/19.
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                                                                                                                                                                                                            8; SEQ ID NO 874; 158pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                         Ouyang
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transformed with two vectors, where the first vector comprises a polynucleotide encoding a first hybrid polypeptide and DNA binding domain and the second vector comprising a polynucleotide encoding a second hybrid polypeptide and an activating domain that activates the toxic reporter gene, when the first and second hybrid polypeptides interact and selecting the modulating compound which inhibits the growth of the recombinant host cell (i.e. using the yeast two-hybrid system). The complexes are useful for identifying compounds that modulate the protein-protein interactions and useful for treating obesity and metabolic disorders e.g. non-insulin dependent diabetes mellitus, NIDDM. The compound isolated by the method is useful for treating and preventing obesity or metabolic diseases. The interactions between the proteins of the complex further define a set of selected interacting company to the proteins of the present sequence represents a member of the protein complex of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rat; yeast two-hybrid assay; adipocyte; bait protein; NIDDM; non-insulin diabetes mellitus; obesity; selected interacting domain; SID; protein-protein interaction map; PIM; anorectic; metabolic disorder.
                                                                                                                                                                                                                                                                                                                                                       interacting polypeptides and a method of selecting a modulating compound in adipocyte cells, by cultivating a recombinant host cell on a selective medium containing a modulating compound and a reporter gene the expression of which is toxic for the recombinant host cell which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel complex of protein-protein interactions in adipocyte cells for identifying compounds that modulate the protein-protein interactions useful for treating obesity and metabolic disorders.
Sequence 410 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a complex of protein-protein interactions (forming a protein-protein interaction map, PIM) in adipocyte cells as defined in the specification, or polynucleotides in adipocytes encoding for the polypeptides. Also included are a recombinant cell expressing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 53; 125pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Legrain P, Marullo S,
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(CNRS ) CENT NAT RECH SCI.
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                                           invention, used
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                                         the bait protein
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                                         the yeast two- hybrid
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ch 2.9%; Score 11; DB cl Similarity 100.0%; Pred. No. 0.: 11; Conservative 0; Mismatches

DB 5; 0.13;

Length 410 Indels

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Sequence

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or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also C claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expressed in an animal subjected to pain, a method for identifying a compound which regulates the expressed in an animal subjected to pain, a method for identifying a compound which regulates the expressed in an animal subjected to pain, a method for identifying a compound that regulates the citivity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a compound that regulates the citivity in an animal of one or more of the polypeptides given in the composition and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that regulates the citivity is useful for preparing a medicament for treating pain and a pharmaceutical nerve injury (Snup), chronic constriction injury (CCI) and spared nerve injury (Snup), in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note:

The sequence data for this patent did not form directly from WIPO at the specification but was obtained in electronic form directly from WIPO at CC fromito.infrub/bublished not arminences.
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01-NOV-2001; 2001US-0346382P
26-NOV-2001; 2001US-0333347P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page; 1017pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New composition comprising two or more isolated polypeptides, useful preparing a medicament for treating pain in an animal.
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2: pir2:*
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beta-arrestin 1 - r
probable signal recognition
nitrogen fixation
protein-tyrosine k
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l - blueb
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RESULT 2 A55081 AF5081 C; Species: Calliphora vicina C; Species: Calliphora vicina C; Species: Calliphora vicina C; Accession: A55081; S44291 R; Plangger, A.; Malicki, D.; Whitney, M.; Paulsen, R. J. Biol. Chem. 269, 26969-26975, 1994 A; Title: Mechanism of arrestin 2 function in rhabdome: A; Reference number: A55081; MUID:95014564; PMID:79294: A; Accession: A55081 A; Status: preliminary A; Molecule type: mRNA	Query Match 5.2%; Score 20; DB 2; Best Local Similarity 100.0%; Pred. No. 3.2e-1 Matches 20; Conservative 0; Mismatches Qy 228 VKKIKAMVQQGVDVVLFQNG 247	A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-364 <hydd- 3="" 306="" 349="" 36="" 3;="" a;cross-references:="" a;gene:="" a;introns:="" arrestin<="" c;genetics:="" c;superfamily:="" flybase:arr1="" flybase:fbgn0000120="" gb:m3014="" th="" uniparc:upi0000000e69;=""><th>A; Status; preliminary A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-364 < SMI> A; Cross-references: UNIPROT: P15372; UNIPARC: UPI0000000E69 A; Cryde, D.R.; Mecklenburg, K.L.; Pollock, J.A.; Vihtelic, R; Hyde, D.R.; Mecklenburg, K.L.; Pollock, J.A.; Vihtelic, Proc. Natl. Acad. Sci. U.S.A. 87, 1008-1012, 1990 A; Title: Twentry Drosophila visual system cDNA clones: one A; Reference number: A34868; MUID: 90138926; PMID: 2105491 A; Accession: A34868</th><th>a melanogaster) cer svision 20-Jul-1990 er, C.S. 7, 1003-1007, 1990 e of an arrestin gen D:90138925; PMID:168</th><th>ALIGNMENTS</th><th>30 7 1.8 92 2 B82603 31 7 1.8 139 2 E97426 32 7 1.8 139 2 E97426 33 7 1.8 139 2 AE2644 34 7 1.8 145 2 C64447 35 7 1.8 145 2 C64447 36 7 1.8 145 2 C64447 37 1.8 151 2 A83639 37 7 1.8 151 2 A83639 37 7 1.8 151 2 C81827 38 7 1.8 151 2 A83639 39 7 1.8 151 2 A83639 40 7 1.8 156 2 A27873 40 7 1.8 166 2 A27873 41 7 1.8 216 2 A95969 42 7 1.8 216 2 A61259 43 7 1.8 216 2 A61259 44 7 1.8 216 2 A61259 45 7 1.8 217 2 B64080 46 7 1.8 231 2 S73469 47 1.8 231 2 A82084</th></hydd->	A; Status; preliminary A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-364 < SMI> A; Cross-references: UNIPROT: P15372; UNIPARC: UPI0000000E69 A; Cryde, D.R.; Mecklenburg, K.L.; Pollock, J.A.; Vihtelic, R; Hyde, D.R.; Mecklenburg, K.L.; Pollock, J.A.; Vihtelic, Proc. Natl. Acad. Sci. U.S.A. 87, 1008-1012, 1990 A; Title: Twentry Drosophila visual system cDNA clones: one A; Reference number: A34868; MUID: 90138926; PMID: 2105491 A; Accession: A34868	a melanogaster) cer svision 20-Jul-1990 er, C.S. 7, 1003-1007, 1990 e of an arrestin gen D:90138925; PMID:168	ALIGNMENTS	30 7 1.8 92 2 B82603 31 7 1.8 139 2 E97426 32 7 1.8 139 2 E97426 33 7 1.8 139 2 AE2644 34 7 1.8 145 2 C64447 35 7 1.8 145 2 C64447 36 7 1.8 145 2 C64447 37 1.8 151 2 A83639 37 7 1.8 151 2 A83639 37 7 1.8 151 2 C81827 38 7 1.8 151 2 A83639 39 7 1.8 151 2 A83639 40 7 1.8 156 2 A27873 40 7 1.8 166 2 A27873 41 7 1.8 216 2 A95969 42 7 1.8 216 2 A61259 43 7 1.8 216 2 A61259 44 7 1.8 216 2 A61259 45 7 1.8 217 2 B64080 46 7 1.8 231 2 S73469 47 1.8 231 2 A82084
#text_change 09-Jul-2004 R. meric photoreceptors. 9436	Length 364; 2; 0; Indels 0; Gaps 0;	0; NID:g156961; PIDN:AAA28380.1; PID:	00B69; GB:M30177 elic, T.S.; Benzer, S. : one is a homolog of human arrestin	#text_change 09-Jul-2004 e from Drosophila. 9056		hypothetical prote hypothetical prote flagellar basal-bo flagellar basal-bo conserved hypothet hypothetical prote hypothetical prote osmotically induci hypothetical prote allophycocyanin al hypothetical prote carQ protein - Myx glycoprotein S - p hypothetical prote probable lipoprote MTA/SAH nucleosida

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RESULT 5
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A;Tille: Arrestin-subtypes in insect antennae.
A;Reference number: A56607; MUID:93199955; PMID:8452755
                                                                                                                                                                                                                                                                                                                                                                                                                                                              arrestin homolog - migratory locust
C;Species: Locusta migratoria (migratory locust)
C;Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 09-Jul-2004
C;Accession: A56607
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A;Experimental source: antennae
A;Note: sequence extracted from NCBI backbone (NCBIP:1279
C;Superfamily: arrestin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Arrestin-subtypes in insect antennae. A;Reference number: A56607; MUID:93199955; PMID:8452755 A;Accession: B56607
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49K photoreceptor protein -
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A; Residues: 1-407 < RAM>
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A; Residues: 1-381 < RAM>
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                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                     A; Contents: antennae
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fruit fly (Drosophila melanogaster)
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arrestin 2 - bluebottle fly (Calliphora vicina)
C;Species: Calliphora vicina
C;Species: Calliphora vicina
C;Date: 08-Uul-1995 #sequence_revision 03-Aug-1995 #text_change 09-Uul-2004
C;Accession: B55081; 844292
R;Plangger, A.; Malicki, D.; Whitney, M.; Paulsen, R.
J. Biol. Chem. 269, 26969-26975, 1994
A;Title: Mechanism of arrestin 2 function in rhabdomeric photoreceptors.
A;Reference number: A55081; MUID:95014564; PMID:7929436
A;Accession: B55081
A;Accession: B55081
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-401 <PLA>
A;Residues: 1-401 <PLA>
A;Cross-references: UNIPROT:P51487; UNIPARC:UPI000016B8DC; EMBL:X79073; NID:g483583; PID
A;Note: the source is designated as Calliphora erythrocephala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Drosophila melanogaster
C;Date: 13-Uul-1990 #sequence_revision 13-Jul-1990 #text_change 09-Jul-2004
C;Accession: A34856
R;Yamada, T.; Takeuchi, Y.; Komori, N.; Kobayashi, H.; Sakai, Y.; Hotta, Y.; Matsumoto, Science 248, 483-485, 1990
A;Title: A 49-kilodalton phosphoprotein in the Drosophila photoreceptor is an arrestin A;Reference number: A34856; MUID:90232360; PMID:2188671
A;Accession: A34856
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C;Date: 21-Nov-1993 #sequence_revision
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A;Cross-references: FlyBase:FBgn0000121
C;Superfamily: arrestin
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A;Residues: 1-401 <YAM>
A;Cross-references: UNIPROT:P19107; UNIPARC:UPI0000126081; GB:M32141; NID:g158157; PIDN:
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A;Introns: 286/1; 351/1
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A; Residues: 1-401 < KRI>
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C; Superfamily: arrestin
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ilarity 100.0%;
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R;Jahns, R.; Borgese, F.; Lindenthal, S.; Straub, A.; Motais, R.; Fievet, B. Biochem. J. 316, 497-506, 1996
A;Title: Trout red blood cell arrestin (TRCarr), a novel member of the arrestin A;Reference number: S68253; MUID:96257743; PMID:8687393
A;Accession: S68253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             arrestin isoform 1S, erythrocyte - rainbow trout
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
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A;Residues: 1-405 <JAH>
A;Cross-references: UNIPROT:P51467; UNIPARC:UPI000012607C; GB:U48410
C;Superfamily: arrestin
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R;Jahns, R.; Borgese, F.; Lindenthal, S.; Straub, A.; Motais, R.; Fievet, B. Biochem. J. 316, 497-506, 1996
A;Title: Trout red blood cell arrestin (TRCarr), a novel member of the arrestin A;Reference number: S68253; MUID:96257743; PMID:8687393
A;Accession: S68254
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S68254
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submitted to the EMBL Data Library, November 1991 A; Description: Isolation of a novel cDNA belonging A; Reference number: S18984
                                                       C;Accession: S18984
R;Rapoport, B.
                                                                                           arrestin - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence
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C;Date: 06-Dec_1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
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Best Local
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Similarity 100.0%; P
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Pred. No.
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Pred. No. 0.0069;
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A;Status: preliminary; not compared with conceptual translation A;Molecule type: mRNA A;Molecule type: mRNA A;Residues: 1-320, 'A',322-325, 'A',327-330, 'A',332-410 <AT2>A;Residues: 1-320, 'A',327-330, 'A',332-410 <AT2>A;Residues: 1-320, 'A',327-330, 'A',332-410 <AT2>A;Residues: 1-320, 'A',327-330, 'A',332-410 <AT2>A;Residues: 1-320, 'A',327-330, 'A',332-410 <AT2>A;Accession: 1-320, 'A',327-330, 'A',332-410 <AT2>A;Accession: 1-320, 'A',327-330, 'A',332-410 <AT2>A;Accession: 1-320, 'A',322-320, 'A',322-320, 'A',332-410 <AT2>A;Accession: 1-320, 'A',322-320, 'A',3
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Jun-2000 #sequence revision 02-Jun-2000 #text_change
C;Accession: A59279; A43404; T70112
R;Attramadal, H.; Arriza, J.L.; Aoki, C.; Dawson, T.M.; Codina, submitted to GenBank, August 1995
A;Reference number: A59279
A;Accession: A59279
A;Accession: A59279
A;Accession: A59279
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A;Title: Beta-arrestin2, a novel member of the arrestin/beta-arrestin gene family.
A;Reference number: A43404; MUID:92388146; PMID:1517224
A;Accession: A43404
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A59279
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A;Molecule type: mRNA
A;Moseidues: 1-409 <RAP>
A;Cross-references: UNIPROT:P32121; UNIPARC:UPI000016A58B; EMBL:Z11501; NID:g28850;
C;Superfamily: arrestin
                                                                                                                                                                                                                                                                                 arrestin isoform 1L, erythrocyte - rainbow trout
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
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R;Jahns, R.; Borgese, F.; Lindenthal, S.; Straub, A.; Motais, Biochem. J. 316, 497-506, 1996
Biochem. J. 316, 497-506, 1996
A;Title: Trout red blood cell arrestin (TRCarr), a novel membe A;Title: number: S68253; MUID:96257743; PMID:8687393
A;Accession: S68255
A;Status: preliminary; nucleic acid sequence not shown
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S68255
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A;Residues: 295-410 <CRA>
A;Cross-references: UNIPARC:UPI0000170BB4; EMBL:U03627; NID:g458202; PIDN:AAA17551.1;
C;Superfamily: arrestin
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A; Residues: 1-410 < ATT>
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100.0%; Pred. No. 0.007;
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C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Date: 16-Feb-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C;Accession: A47140; B47140; JC2051
R;Sterne-Marr, R.; Gurevich, V.V.; Goldsmith, P.; Bodine, R.C.; Sanders, C.
J. Biol. Chem. 268, 15640-15648, 1993
A;Title: Polypeptide variants of beta-arrestin and arrestin3.
A;Reference number: A47140; MUID:93340166; PMID:8340388
A;Accession: A47140
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A;Residues: 1-415 <JAH>
A;Cross-references: UNIPROT:P51468; UNIPARC:UPI000012607E; GB:U48410
C;Superfamily: arrestin
                                                                                                                                                                                                                                                          C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_
C;Accession: I55423
R;Craft, C.M.; Whitmore, D.H.; Wiechmann, A.F.
J. Biol. Chem. 269, 4613-4619, 1994
A;Reference number: I55423; MUID:94140898; PMID:8308033
A;Accession: I55423; MUID:94140898; PMID:8308033
A;Accession: I55423; MUID:94140898; PMID:8308033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;ACCEBBALVII. - - MRNA
A;Molecule type: mRNA
A;Residues: 1-362,374-420 <ST2>
A;Cross-references: UNIPARC:UPI0000178BC3
A;Cross-references: UNIPARC:UPI0000178BC3
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A; Residues: 1-387 < RES>
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F;1-362,374-420/Product: arrestin arr3S #status predicted <MA2>
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A;Accession: B47140
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A;Experimental source: brain
                                                                                  Query Match
Best Local S
Matches 9
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                                GKRDFVDHV 30
          GKRDFVDHV
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                                                                                2.3%; Score 9; ilarity 100.0%; Pred. No. Conservative 0; Mismatc
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llarity 100.0%;
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          27
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o. 0.77;
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RESULT 15
S38943
Search completed: May 20, 2006, 23:16:16
Job time: 42 secs
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                                                                                                                                                                                                                                                                                                                                                                                                            arrestin - human
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence
C;Accession: S38943
                                                                                                                                                                                                                       C; Superfamily: arrestin
                                                                                                                                                                                                                                          A;Cross-references: UNIPROT: P36575; UNIPARC: UP1000004230C; GB: S66793; NID: g439830; PIDN: I
                                                                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-388 <MUR>
                                                                                                                                                                                                                                                                                                                                                                       R;Murakami, A.; Yajima, T.; Sakuma, H.; McLaren, M.J.; Inana, FEBS Lett. 334, 203-209, 1993
                                                                                                                                                 Matches
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Best Local
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                                                                                                            22 GKRDFVDHV 30
                                                                                                                                               Similarity 9; Conserv
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                                                                                                                                             2.3%; So ilarity 100.0%; I Conservative 0;
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Post-processing: Listing first 45
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score greater than or equal to the score of the result being printed,
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Q95NF3_ANOGA
Q6VPPO_ANOGA
Q5TNW2_ANOGA
Q9BIG9_9NEOP
ARRA_DROME
Q7YTTV9_ANOST
Q7YTTV9_ANOAR
Q3TRČB MOUSE
ARRZ_ONCMY
Q5FDD MOUSE
Q6FFK2_BRARE
ARRI_ONCMY
Q6DFC4_XENLA
Q6GFY2_XENLA
Q7T2D2_BRARE
ARRB2_HUMAN
Q2FP19_HUMAN
Q6ICT3_HUMAN
                                                                                                                                                                                             ARRH—HELVI
Q6XIZ6 DROYA
ARRH LIMPO
ARRH—LOCMI
Q68DZ5 HUMAN
Q58IJ0_DROME
Q7Q5Q8_ANOGA
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ARRB DROMI
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Q7q5q8
P51487
P19108
P31cc8
P512d9
Q6pfk2
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6 oncorhynchu
4 xenopus lae
2 xenopus lae
2 brachydanio
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9 homo sapien
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7 calliphora
7 drosophila
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Result No.

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	Q5rcr4 pongo pygma Q91yi4 mus musculu P29067 rattus norv Q59em5 homo sapien Q31cm2 mus musculu Q5f2e0 m novel pro P51468 oncorhynchu P32120 bos taurus Q5f2d8 mus musculu Q6wgr2 metapenaeus Q4v8r0 brachydanio Q4spt4 tetraodon n Q5xj55 brachydanio Q5f223 homo sapien

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GO; GO:0007600; P:sensory perception; IE;
GO; GO:0007165; P:signal transduction; II
InterPro; IPR001028; Arrestin C.
InterPro; IPR011022; Arrestin N.
InterPro; IPR011021; Arrestin N.
PANTHER; PTHR11792; Arrestin; 1.
Pfam; PF02752; Arrestin C; 1.
Pfam; PF02732; Arrestin_N; 1.
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Q55NF3 ANOGA
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Q1-DEC-2001,
01-DEC-2001,
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"Molecular characterization and chromosomal mapping of transcripts
having tissue-specific expression in the malaria mosquito anopheles
gambiae: possible involvment in visual or olfactory processes.";
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
Anophelinae; Anopheles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21819361; PubMed=11792843; DOI=10.1073/pnas.022505499; Merrill C.E., Riesgo-Escovar J., Pitts R.J., Kafatos F.C.,
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MEDLINE=21680430; PubMed=11822731; DOI=10.1007/s00436-002-0637-0;
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea, Culicidae,
Anophelinae, Anopheles.
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Morlais I., Poncon N., Simard F., Cohuet A., 1
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ
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Neophelinae; Anopheles
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07-EBC, entry version 7.
ENSANGP0000027511 (Fragment).
ORFNames=ENSANGG00000010080;
                                                            GO; GO:0007600; P:sensory perception; IEA. GO; GO:0007165; P:signal transduction; IEA. InterPro; IPR000698; Arrestin. InterPro; IPR011022; Arrestin C. InterPro; IPR011021; Arrestin N. PANTHER; PTHR11792; Arrestin; 1.
                                                                                                                                                                                                                                                 Copyrighted by the UniProt Consortium, Distributed under the Creative Commons
                                                                                                                                                                                                                                                                                                                                                The Anopheles gambiae Sequence Committee;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry v
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                   PF02752; Arrestin_C; 1. PF00339; Arrestin_N; 1.
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GO; GO:0007165; P:signal transduction; IEA
GO; GO:0007165; P:signal transduction; IEA
InterPro; IPR001022; Arrestin C.
InterPro; IPR011022; Arrestin N.
InterPro; IPR011021; Arrestin I.
PANTHER; PTHR11792; Arrestin I.
Pfam; PF02752; Arrestin C; 1.
Pfam; PF02752; Arrestin N; 1.
PFRNTYS; PR00309; ARRESTIN.
PROSITE; PR003095; ARRESTINS; 1.
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01-JUN-2001,
07-FEB-2006,
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Neuroptera; Ascalaphidae; Ascalaphus
NCBI_TaxID=146496;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21184354; PubMed=11287006; DOI=10.1016/S0014-5793(01)02287-6; Bentrop J., Schillo M., Gerdon G., Draslar G., Paulsen R.; "UV-light-dependent binding of a visual arestin 1 isoform to
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HSSP; P17870; 1G4M.
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; PS00295; ARRESTINS; 1
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                                                                                                             Similarity
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                              RKVFGQIVCSFRYGREEDEVMGLNF
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  RKVFGQIVCSFRYGREEDEVMGLNF
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llarity 100.0%;
Conservative (
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30553 MW;
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                                                                                        Score 25; DB; Pred. No. 1e-
0; Mismatches
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                                                                                                                                                                                   451DEF465969857D CRC64;
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IEA.
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Attribution-NoDerivs License
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RESULT
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RA Adams M.D., Celniker S.E., Hilt R.M., Howkins R.A., Golayer J.D.,
RA Adams M.D., Celniker S.E., Hilt R.M., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Barlew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Barlew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Gerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Gerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Gerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Gerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Gerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Gerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Gerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Gerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Gerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Gerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kratt C., Krautz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kratt C., Krautz S., Kulp D., Lai Z.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Harris N.M., Packer J., Sanders R.D.C., Scheeder F., Shen H.,
RA Harris M.R., Woodage T., Worter E., Wang S., Yao Q.A.,
RA Marris S.M., Woodage T., Worter E., Wung S., Zhu X., Smit
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MEDLINE-90138925; PubMed-168955;
Smith D.P., Sheih B.-H., Zuker C.S.;
"Isolation and structure of an arrestin gene fro
Proc. Natl. Acad. Sci. U.S.A. 87:1003-1007(1990)
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Hyde D.R., Mecklenburg K.L., Pollock J.A., Vihteli
"Twenty Drosophila visual system cDNA clones: one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Berkeley;
MEDLINE=20196006;
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       GENOME REANNOTATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=10731132; DOI=10.1126/science.287.5461.2185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [LARGE SCALE GENOMIC DNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    into UniProtKB/Swiss-Prot
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A) (Arrestin-1).
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Intact; 195372; -...
Ensembl; CG5711; Drosophila melanogaster.
FlyBase; FBgn000120; Arr1.
BioCyc; DMEL-XXX-02:DMEL-XXX-02-009314-MONOMER; -..
GO; GO:0005624; C:membrane fraction; IDA.
GO; GO:0016028; C:rhabdomere; IDA.
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0016600; P:metarhodopsin inactivation; IGI.
InterPro; IPR000698; Arrestin.
                                                                                                                                                                                                                                      EMBL; M30177; -; NOT ANNOTATED_CDS; Genomic_DNA.
EMBL; M30140; AAA28380.1; -; Genomic_DNA.
EMBL; AE00357; AAF33644.1; -; Genomic_DNA.
EMBL; AX061824; AAL27635.1; -; mRNA.
PIR; A34867; A34867.
HSSP; P17870; 1G4M.
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Rubin G.M., Celniker S.E.;
"A Drosophila full-length cDNA resource.";
"A Drosophila full-length cDNA resource.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stapleton M., Carrin H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                  Copyrighted Distributed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matsumoto H., Yamada T.;
"Phosrestins I and II: arrestin blight_induced phosphorylation in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Berkeley; TISSUE=Head;
MEDLINE=22426066; PubMed=12537569;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=93303590; PubMed=8316831;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochem.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Arrestin function in inactivation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ewis S.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERACTION:

(QSVIM6:CG10949; NDExp=1; IntAct=EBI-145156, EBI-153699;

QSVAP2:CG11881; NDExp=1; IntAct=EBI-145156, EBI-186540;

QSVAP2:CG11881; NDExp=1; IntAct=EBI-145156, EBI-151455;

QSVAP2:CG12155; NDExp=1; IntAct=EBI-145156, EBI-151455;

QSVAP3:CG3754; NDExp=1; IntAct=EBI-145156, EBI-160250;

QSVAP1:CG3995; NDExp=1; IntAct=EBI-145156, EBI-160250;

QSVAP1:CG395; NDExp=1; IntAct=EBI-145156, EBI-16076;

QSVAP1:CG395; NDExp=1; IntAct=EBI-145156, EBI-15350;

TISSUE SPECIFICITY: Expressed specifically and abundantly in the photoreceptore. Inner and outer segments, and the inner plexiform regions of the retina.

THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE PROSPECTION OF THE
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SIMILARITY: Belongs to the arrestin family.
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Pfam; PF003752; Arrestin N; 1.
Pfam; PF00339; Arrestin N; 1.
PRINTS; PR00399; ARRESTIN.
ProDom; PD002099; Arrestin; 2.
PROSITE; PS002095; ARRESTINS; 1.
PROSITE; PS002095; ARRESTINS; 1.
Complete proteome; Phosphorylation; Sensory transduction; Vision.
COMPLET (CALIN ) 1 354
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01-OCT-2003, integrated int
01-OCT-2003, sequence versi
07-FEB-2006, entry version
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Favia G., ricci I., Casiraghi M., Esposito F.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anopheles stephensi (Indo-Pakistan malaria mosquito).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Cul
Anophelinae; Anopheles; stephensi species complex.
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PANTHER; PTHR11792; Arrestin; 1.
                                                                                               Anopheles pharoensis.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Cul
Anophelinae; Anopheles.
                                                                                                                                                                                                   Name=arr1;
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01-OCT-1996; g
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Phosrestin-2
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                                                                                   Calliphora vicina (Blue blowfly) (Calliphora erythrocephala).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oe:
Calliphoridae; Calliphora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AJ544225; CAD66650.1; -; Genomic_DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anopheles arabiensis (Mosquito).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
Anophelinae; Anopheles.
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MEDLINE=95014564; PubMed=7929436;
Plangger A., Malicki D., Whitney M.,
"Mechanism of arrestin 2 function in
                                                                                                                                          Name=ARR1;
                                                                                                                                                                                                                                                                                                                                                                                   SEQÜENCE 18 AA; 2075 MW;
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Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases
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                                     TISSUE=Retina
                                                  NUCLEOTIDE SEQUENCE
                                                                         NCBI_TaxID=7373;
                                                                                                                                                                                                                  ARR1_CALVI
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Pfam; PF00339; Arrestin_N; 1.
PRINTS; PR00309; ARRESTIN.
PRODOM; PD002099; Arrestin; 2.
PROSITE; PS00295; ARRESTINS; 1.
Sensory transduction; Vision.
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HSSP; P17870; 1G4M.
InterPro; IPR0100698; Arrestin.
InterPro; IPR011022; Arrestin_C.
InterPro; IPR011021; Arrestin_N.
PANTHER; PTHR11792; Arrestin; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=9319995; PubMed=8452755; DOI=10.1016/0898-6568(93)90009-B; Raming K., Freitag J., Krieger J., Breer H.; "Arrestin-subtypes in insect antennae."; Cell. Signal. 5:69-80(1993).
-!- SIMILARITY: Belongs to the arrestin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X79072; CAA55672.1; -; mRNA.
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noc
Noctuidae; Heliothinae; Heliothis.
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PRINTS; PR00309; ARRESTIN,
ProDom; PD002099; Arrestin; 2
PROSITE; PS00295; ARRESTINS;
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PANTHER; PTHR11792; Arrestin; 1.
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RESULT 13
ARRH LIMPO
ID ARRH LI
AC P51464
AC P51467
DT 01-OCT
DT 01-OCT
DT 01-FEB
DE Arrest
OS Limulu
OC Eukary
OC Limuli
OC Eukary
RN [1]
RN [1]
RN [1]
RN [1]
RN [1]
RN SMith
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                                                                                                                                        ARRH LIMPO
P51484;
01-OCT-1996,
01-OCT-1996,
(1)

NUCLEOTIDE SEQUENCE [MRNA].

TISSUB=Retina;

TISSUB=95096819; PubMed=7798902;

MEDLINE=95096819; PubMed=7798902;
                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0007600; P:sensory perception; I
GO; GO:0007165; P:signal transduction;
InterPro; IPR000698; Arrestin.
InterPro; IPR011021; Arrestin.N.
PANTHER; PTHR11792; Arrestin; 1.
Pfam; PF00339; Arrestin; 1.
ProDom; PD002099; Arrestin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-UUL-2004, integrated into UniProtKB/TrEMBL.
05-UUL-2004, sequence version 1.
07-FBB-2006, entry version 8.
Similar to Drosophila melanogaster CG5711 (Fragment)
                                                                          Limulus polyphemus (Atlantic horseshoe
Eukaryota; Metazoa; Arthropoda; Chelice
Limulidae; Limulus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Copyrighted by the UniProt Consortium, see http://www.uniprot.org/termsDistributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22887302; PubMed=14525923; DOI=10.1101/gr.1311003; Domazet-Loso T., Tautz D.; Domazet-Loso T., Tautz D.; "An evolutionary analysis of orphan genes in Drosophila."; Genome Res. 13:2213-2219(2003).
                                                             NCBI_TaxID=6850;
                                                                                                                Arrestin,
                                                                                                                            07-FEB-2006,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P08168; 1AYR.
FlyBase; FBgn0068531; Dyak\Arr1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AY232006; AAR10029.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=7245;
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                                                                                                                                                                                                                                                                                              14;
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                                                                                                                lateral eye
                                                                                                                                                                                                                                                                                                                                              52 AA;
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                                                                                                                                                                                                                                                                                                                                                            52
                                                                                                                              entry version
                                                                                                                               entry version 26.
                                                                                                                                                       integrated into UniProtKB/Swiss-Prot
                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                              6166 MW; 081C148570B5EB6F CRC64;
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Pred. No.
                                                                                         rseshoe crab).
Chelicerata; Merostomata; Xiphosura;
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  B.G.,
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o. 1.9e-05;
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   Hendrix M.M.,
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era; Muscomorpha;
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      Hutchinson
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RESULT 14
ARRH LIA
ID ARRH LIA
AC P32122
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Best Local :
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InterPro; IPRO11022; Arrestin_C.
InterPro; IPRO11021; Arrestin_N.
PANTHER; PTHR11792; Arrestin_T.
Pfam; PF02752; Arrestin_C; 1.
Pfam; PF00339; Arrestin_N; 1.
PfANTS; PR00309; ARRESTIN.
ProDom; PD002099; ARRESTIN.
PROSSITE; PS00299; ARRESTINS; 1.
PROSSITE; PS00299; ARRESTINS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -ARRH_LOCMI STANDARD;
P32122;
01-OCT-1993, integrated into
01-CCT-1995, sequence versio
07-FEB-2006, entry version 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Locusta migratoria (Migratory locust).

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
Acridoidea; Acrididae; Oedipodinae; Locusta.

NCBI_TaxID=7004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Phosphorylation; Sensory transduction; Vision.
CHAIN
1 400 Arrestin, lateral eye.
FTId=PRO 0000205219.
SEQUENCE 400 AA; 44302 MW; F30D0D25BC2BEE33 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Neurochem. 64:1-13(1995).
                                                                                                                                                                                                                                                                                                                    Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=93199955; PubMed=8452755; DOI=10.1016/0898-6568(93)90009-B; Raming K., Frettag J., Krieger J., Breer H.; "Arrestin-subtypes in insect antennae."; Cell. Signal. 5:69-80(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arrestin homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U08883; AAA82007.1; -; mRNA.
HSSP; P17870; 1G4M.
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                                                                                                                                                                                                            EMBL; S57174; AAB25860.1; -; mRNA
PIR; A56607; A56607.
HSSP; P17870; 1G4M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE [MRNA].
  PRINTS; PR00309; ARRESTĪN.
ProDom; PD002099; Arrestin; 2.
                                                                                                       InterPro; IPR000698; Arrestin.
InterPro; IPR011022; Arrestin N.
InterPro; IPR011021; Arrestin N.
InterPro; PTHR11792; Arrestin; 1.
                                                   Pfam; PF02752; Arrestin_C; 1.
Pfam; PF00339; Arrestin_N; 1.
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SIMILARITY: Belongs to the arrestin
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13; Conserv
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Pred. No.
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Search completed: May 20, Job time: 302 secs

2006,

23:15:29

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RESULT 15
Q68DZ5_HUMAN
ID Q68DZ5_H
AC Q68DZ5;
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                                                                                     ProDom; PD002099; Arrestin; 1.
Hypothetical protein.
SEQUENCE 217 AA; 24363 MW;
                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                   Ottenwaelder B., Obermaier B., Deutschenbaur S., Schaipp
Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M
Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                    SMR;
                                                                                                                                                                                                                                                                                                                                                                                                                               11-OCT-2004,
07-FEB-2006,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sensory transduction. CHAIN 1 40
                                                                                                                     Ensembl; ENSG00000141480; Homo sapiens.
GO; GO:0007600; P:sensory perception; IEA.
GO; GO:0007165; P:signal transduction; IEA.
InterPro; IPR000698; Arrestin
InterPro; IPR011022; Arrestin
PANTHER; PTHR11792; Arrestin; 1.
Pfam; PF02752; Arrestin; 1.
                                                                                                                                                                                                                                     Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein DKFZp686L0365 Name=DKFZp686L0365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q68DZ5_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                     The German cDNA Consortium;
                                                                                                                                                                                                                                                                                                                  TISSUE=Endometrium;
                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE
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147
                     341
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                                                                                                                                                                                                               CR749218; CAH18075.1; -; mRNA.
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/EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
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US-09-980-137-3

US-09-880-137-2

US-09-880-137-2

US-09-641-528B-20523

US-09-641-528B-31963

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ALIGNMENTS

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APPLICANT: Berstein, Gabriel
TITLE OF INVENTION: METHODS OF ASSAYING FOR G
TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIC
FILE REFERENCE: MNI-131
CURRENT APPLICATION NUMBER: US/09/880,137
CURRENT FILING DATE: 2001-03-05
CURRENT FILING DATE: 2000-03-05
PRIOR APPLICATION NUMBER: US 60/186,706
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 409
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CURRENT APPLICATION NUMBER: US/09/880,137
CURRENT FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: US 60/186,706
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEO ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEO ID NO 8
LENGTH: 382
TYPE: PRT
ORGANISM: Artificial Sequence
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US-09-880-137-4
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PATENT NO. 6640025
GENERAL INFORMATION:
APPLICANT: Berstein, Gabriel
APPLICANT: Berstein, Gabriel
TITLE OF INVENTION: METHODS OF ASSAYING FOR G
TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
                                                                                                                                                                                                                                                                  Patent No. 6640025
GENERAL INFORMATION:
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Best Local Similarity
Matches 11; Conserv
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; ORGANISM: Homo 8
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US-09-880-137-5
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PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 7
                                                                                                                                                                                           APPLICANT: Berstein, Gabriel
APPLICANT: Berstein, Gabriel
TITLE OF INVENTION: METHODS OF ASSAYING FOR G
TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
FILE REFERENCE: MNI-131
CURRENT FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: US/09/880,137
CURRENT FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: US 60/186,706
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
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APPLICANT: BEFSELEIN, GABRIEL
TITLE OF INVENTION: METHODS OF ASSAYING FOR G
TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
FILE REFERENCE: MNI-131
CURRENT APPLICATION UNMERS: US/09/880,137
CURRENT FILING DATE: 2001-03-05
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Matches
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Patent No. 66400
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ORGANISM: Homo sapiens
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TYPE: PRT
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Local Similarity 100.0%; Pred. No.
les 11; Conservative 0; Mismatch
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les 9; Conserv
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         GKRDFVDHV
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100.0%; Pred. No. 0.037;
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 27414
LENGTH: 279
TYPE: PRT
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Best Local Similarity
Watches 9; Conserv:
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TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-137-6
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US-09-880-137-6
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                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-27414
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Patent No. 6640025

GENERAL INFORMATION:
APPLICANT: Berestein, Gabriel
TITLE OF INVENTION: METHODS OF ASSAYING FOR G
TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
FILE REFERENCE: MNI-131
             Sequence 9940, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 6551795
GENERAL INFORMATION:
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Best Local (
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Patent No. 6551795
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CURRENT FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: US 60/186,706
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/949,016
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8; Conserva
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llarity 100.0%;
Conservative
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100.0%; Pred. No. 22
tive 0; Mismatches
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                                     ASSOCIATED
OF DETECTION AND USES THEREOF
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PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR PRIOR PRIOR DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8383
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; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9940
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US-09-949-016-8384
; Sequence 8384, Application US/09949016
natent No. 6812339
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Best Local Similarity
Watches 8; Conserva
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PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION UNMERR: US/09/949,016
CURRENT APPLICATION TOMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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                            APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE:
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Local Similarity 100.0%; Pred. No. 24;
les 8; Conservative 0; Mismatches
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2000-10-03
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Pred. No.
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o. 30;
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; LENGTH: 401
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8384
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-137-3
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US-09-880-137-1
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US-09-880-137-3
                                                                                     US-09-880-137-1
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CURRENT FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: US 60/186,706
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 3
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GENERAL INFORMATION:
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Query Match
Best Local Similarity 100.0%;
Matches 8; Conservative (
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APPLICANT: Berstein, Gabriel
APPLICANT: Berstein, Gabriel
TITLE OF INVENTION: METHODS OF ASSAYING FOR G
TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
FILE REFERENCE: MNI-131
FILE REFERENCE: MNI-131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Patent No. 6640025
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Best Local Similarity 100.0%;
Matches 8; Conservative (
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Best Local Similarity
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CURRENT FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: US 60/186,706
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 8
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PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
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TITLE OF INVENTION: METHODS OF ASSAYING FOR G
TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
FILE REFERENCE: MNI-131
                                                                                                 LENGTH: 418
TYPE: PRT
ORGANISM: Bos taurus
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100.0%; Pred. No. 31
1ve 0; Mismatches
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US-09-880-137-2

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SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 418
TYPE: PRT
ROANISM: Homo sapiens
US-09-880-137-2
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                                                         Query Match
Best Local Similarity
Thes 7; Conservat
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Patent No. 6640025
GENERAL INFORMATION:
APPLICANT: Berselein, Gabriel
TITLE OF INVENTION: METHODS OF ASSAYING FOR G
TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
FILE REFERENCE: MUI-131
CURRENT APPLICATION NUMBER: US/09/880,137
CURRENT FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: US/09/86,706
PRIOR PRILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 8
SOFTWARPE: Fastero for withdams Vaccious
                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR FILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 51505
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2512
LENGTH: 8
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APPLICANT: Sidney, John
APPLICANT: Southmood, Scott
APPLICANT: Southmood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Celis, Esteban
APPLICANT: Grey, Howard
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
FILE REFERENCE: 2060.0100001
CURRENT APPLICATION NUMBER: US/09/641,528B
CURRENT APPLICATION NUMBER: US/09/641,528B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No.
                                                                                                                                                                                OTHER INFORMATION: Peptide Derived from Human Papillomavirus
                                                                                                                                                                                                     ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                               TYPE: PRT
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Local Similarity 100.0%; Pred. No. 31
Les 8; Conservative 0; Mismatches
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Sequence 20553, Application US/09641528B
Patent NO. 7026443
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Celis, Esteban
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APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Chesnut, Robert
APPLICANT: Cells, Esteban
APPLICANT: Grey, Howard
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US-09-641-528B-31963
; Sequence 31963, Application US/09641528B
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Matches 7
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SEQ ID NO 20553
LENGTH: 8
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APPLICANT: Chesnut, Robert
APPLICANT: Celis, Esteban
APPLICANT: Grey, Howard
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
FILE REFERENCE: 2060.010001
CURRENT APPLICATION NUMBER: US/09/641,528B
CURRENT FILING DATE: 2000-08-15
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PRIOR FILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 51505
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APPLICANT: Celis, Esteban
APPLICANT: Grey, Howard
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
FILE REFERENCE: 2060.0100001
                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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Search completed: May 20, 2006, 23:17:11 Job time : 50 secs

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Match Length
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1: /BMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

4: /BMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*
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US-99-800-137A-9

US-10-094-240-27

US-11-097-143-12684

US-99-800-137A-7

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ALIGNMENTS

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Sequence 2, Application US/10094240

Publication No. US20030082637A1

GENERAL INFORMATION:
APPLICANT: ZWIEBEL, LAURENCE J.
TITLE OF INVENTION: ARRESTIN GENE, POLYPEPTIDE, ANI
FILE REFERENCE: N8289

CURRENT APPLICATION NUMBER: US/10/094,240

CURRENT FILING DATE: 2001-03-08

PRIOR APPLICATION NUMBER: 10/056,405

PRIOR APPLICATION NUMBER: 60/264,649

PRIOR APPLICATION NUMBER: 60/264,649

PRIOR APPLICATION NUMBER: 00/264,649

PRIOR FILING DATE: 2001-01-26

NUMBER OF SEQ ID NOS: 27

CONTRIANDE: DATE: 2001-01-26

NUMBER OF SEQ ID NOS: 27
                                                                                                                                                                                                                                                                                                                                                                                                       ; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Anopheles gambiae
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                                                                                                                                                                                                                    RESULT 3
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Publication No. US20030166013A1
GENERAL INFORMATION:
APPLICANT: ZWIEBEL, LAURENCE J.
TITLE OF INVENTION: MOSQUITO OLFACTORY GENES, POLYPEPTIDES,
TITLE OF INVENTION: USE THEREOF
                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                    Sequence 238, Application US/10954778 Publication No. US20050153368A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 383; DB Best Local Similarity 100.0%; Pred. No. 0; Matches 383; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: N7841
CURRENT APPLICATION NUMBER: US/10/056,405
CURRENT FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: 60/264,649
PRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin Ver. 2.1
APPLICANT: ZWIEBEL, LAURENCE J.

TITLE OF INVENTION: METHOD OF IDENTIFYING CHEMICAL AGENTS WHICH STIMULATE TITLE OF INVENTION: ODORANT RECEPTORS OF SENSORY NEURONS FILE REFERENCE: N1125

CURRENT APPLICATION NUMBER: US/10/954,778

CURRENT FILING DATE: 2004-09-30

PRIOR APPLICATION NUMBER: 10/056,405

PRIOR APPLICATION NUMBER: 60/264,649

PRIOR APPLICATION NUMBER: 60/264,649
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     Query Match
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; PRIOR FILING DATE: 2001-01-26;
; NUMBER OF SEQ ID NOS: 248;
; SOFTWARE: PATENTIN Ver. 3.3;
; SEQ ID NO 238;
; LENGTH: 383;
; TYPE: PRT;
; ORGANISM: Anopheles gambiae
US-10-954-778-238
                                                                                                                                                                                                                Sequence 18, Application US/10745237

Publication No. US20050227301A1

GENERAL INFORMATION:
APPLICANT: Cyclacel Limited
APPLICANT: Glover, David
APPLICANT: Bell, Graham
APPLICANT: Bell, Graham
APPLICANT: Midgley, Carol
TITLE OF INVENTION: Cell Cycle Progression Proteins
FILE REFERENCE: P01581990 CYK
CURRENT APPLICATION NUMBER: US/10/745,237
CURRENT FILING DATE: 2003-01-10
PRIOR APPLICATION NUMBER: US 60/439,123
PRIOR APPLICATION NUMBER: US 60/468,402
PRIOR FILING DATE: 2003-05-06
NUMBER OF SEQ ID NOS: 660
NUMBER OF SEQ ID NOS: 660
NUMBER OF SEQ ID NOS: 660
; OTHER INFORMATION: US-10-745-237-18
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                                                                                                                                    SOFTWARE: PatentIn version 3.1
SEQ ID NO 18
LENGTH: 364
TYPE: PRT
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Best Local Similarity
Matches 383; Conserv
                                                                  FEATURE:
OTHER INFORMATION:
                                                                                                          ORGANISM: Drosophila melanogaster
                                               FEATURE:
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Pred. No. 0;
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RESULT 5
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CURRENT APPLICATION NUMBER: US/11/097,143

CURRENT FILING DATE: 2005-04-04

PRIOR APPLICATION NUMBER: 60/157,832

PRIOR FILING DATE: 1999-10-05

PRIOR APPLICATION NUMBER: 60/160,191

PRIOR FILING DATE: 1999-10-19

PRIOR FILING DATE: 1999-10-19

PRIOR FILING DATE: 1999-10-28

PRIOR FILING DATE: 1999-10-28
                                                                                                                   GENERAL INFORMATION:
APPLICANT: Berstein, Gabriel
TITLE OF INVENTION: METHODS OF ASSAYING FOR G
TITLE OF INVENTION: METHODS OF ASSAYING FOR G
TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
FILE REFERENCE: MNI-131
CURRENT FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: US 60/186,706
PRIOR FILING DATE: 2000-03-03
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Publication No. US20050208558A1
GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 12000
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Best Local Similarity
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                                                        NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
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APPLICANT: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS
TITLE OF INVENTION: ARRAYS, FOR DETECTING
TITLE OF INVENTION: DROSOPHILA GENES.
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PRIOR
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PRIOR APPLICATION NUMBER: 60/191,637
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                       LENGTH: 382
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FILING DATE: 1999-11-12
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APPLICATION NUMBER: 60/175,693
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100.0%; Pred. No. 3.4e-10
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EXPRESSION OF 10,000 OR MORE
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CURRENT APPLICATION NUMBER: US/09/800,137A
CURRENT FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: US 60/186,706
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
SEQ ID NO 8
SEQ TYPARE: PART
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Homo sapiens mutation
US-09-800-137A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Description of Artificial Sequence: Homo US-09-880-137-8
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                                                                         ; ORGANISM: Anopheles gambiae US-10-094-240-25
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US-10-094-240-25
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Publication No. US20030157553A1

GENERAL INFORMATION:
APPLICANT: Berstein, Gabriel
TITLE OF INVENTION: METHODS OF ASSAYING FOR G
TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
FILE REFERENCE: MNI-131
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Best Local Similarity
Matches 11; Conserv
                                                                                                           SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 25
LENGTH: 398
TYPE: PRT
                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:

APPLICANT: ZWIEBEL, LAURENCE J.

TITLE OF INVENTION: ARRESTIN GENE, POLYPEPTIDE, AND METHODS OF USE THEREOF FILE REFERENCE: N8289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.9%;
Best Local Similarity 100.0%;
Matches 11; Conservative
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   Matches
               Query Match
Best Local Similarity
                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/094,240
CURRENT FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: 10/056,405
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: 60/264,649
PRIOR APPLICATION NUMBER: 60/264,649
PRIOR FILING DATE: 2001-01-26
                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 27
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11;
2.9%; Score 11; DB 4; ilarity 100.0%; Pred. No. 0.16; Conservative 0; Mismatches
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62 RYGREEDEVMG 72

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61 RYGREEDEVMG

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Sequence 27, Application US/10094240

Publication No. US20030082637A1

GENERAL INFORMATION:
APPLICANT: ZWIEBEL, LAURENCE J.

ITILE OF INVENTION: ARRESTIN GENE, POLYPEPTIDE, AND METHODS OF 1

FILE REFERENCE: N8289

CURRENT APPLICATION NUMBER: US/10/094,240

CURRENT FILING DATE: 2001-03-08

PRIOR APPLICATION NUMBER: 10/056,405

PRIOR APPLICATION NUMBER: 60/264,649

PRIOR FILING DATE: 2002-01-26

NUMBER OF EGG ID NOS: 27

SOFTWARE: PatentIn Ver. 2.1

SECTUM 0 27

LENGTH. 407
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PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: 60/264,649
PRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 248
SOFTWARE: Patentin Ver. 3.3
SEQ ID NO 241
                                                                                                    US-11-097-143-12684
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TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-094-240-27
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US-10-094-240-27
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TYPE: PRT
; ORGANISM: Anopheles gambiae
US-10-954-778-241
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US-10-954-778-241
                                                                                                                            RESULT 11
Sequence 12684, Application US/11097143
Publication No. US20050208588A1
GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
APPLICANT: et al.
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APPLICANT: ZWIEBEL, LAURENCE J.
APPLICANT: ZWIEBEL, LAURENCE J.
TITLE OF INVENTION: METHOD OF IDENTIFYING CHEMICAL AGENTS WHICH STIMULATE
TITLE OF INVENTION: ODORANT RECEPTORS OF SENSORY NEURONS
TILE REFERENCE: N1115
CURRENT APPLICATION NUMBER: US/10/954,778
CURRENT FILING DATE: 2004-09-30
CURRENT FILING DATE: 2004-09-30
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Best Local Similarity
Matches 11; Conserv
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Best Local
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1 Similarity 100.0%; P
11; Conservative 0;
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; Pred. No. 0.16;
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-137-4
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CURRENT APPLICATION NUMBER: US/11/097,143

CURRENT FILING DATE: 205-04-04

PRIOR APPLICATION NUMBER: 60/157,832

PRIOR FILING DATE: 1999-10-05

PRIOR FILING DATE: 1999-10-19

PRIOR PRIOR DATE: 1999-10-29

PRIOR APPLICATION NUMBER: 60/161,932

PRIOR PRILING DATE: 1999-10-28

PRIOR PRILING DATE: 1999-10-28

PRIOR PILING DATE: 1999-11-2

PRIOR APPLICATION NUMBER: 60/164,769

PRIOR APPLICATION NUMBER: 60/173,383

PRIOR PILING DATE: 1999-11-2

PRIOR APPLICATION NUMBER: 60/175,693

PRIOR PILING DATE: 2000-01-12

PRIOR APPLICATION NUMBER: 60/184,831

PRIOR PILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: 60/184,831

PRIOR APPLICATION NUMBER: 60/184,831

PRIOR APPLICATION NUMBER: 60/184,831

PRIOR APPLICATION NUMBER: 60/184,831

PRIOR APPLICATION NUMBER: 60/184,831

PRIOR APPLICATION NUMBER: 60/184,831

PRIOR APPLICATION NUMBER: 60/184,831

PRIOR PILING DATE: 2000-02-24

PRIOR PILING DATE: 2000-03-23

NUMBER OF SEO IT NOS: 43008
                                                                      Query Match
Best Local Similarity 100.0%;
Matches 11; Conservative (
                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Berstein, Gabriel
TITLE OF INVENTION: METHODS OF ASSAYING FOR G
TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
FILE REFERENCE: MNI-131
CURRENT APPLICATION NUMBER: US/09/880,137
CURRENT FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: US 60/186,706
PRIOR APPLICATION NUMBER: US 60/186,706
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FASTSEQ for Windows Version 4.0
150CTUN 04
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12684
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Matches
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Patent No. US20020031295A1
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TYPE: PRT
  339
                            341 ELPFVLMHPKP 351
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11; Conserv
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ELPFVLMHPKP 349
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RESULT 13 US-09-880-137-7 ; Sequence 7, Application US/09880137 ; Patent No. US20020031295A1

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; TYPE: PRT; ORCANISM: Artificial Sequence; PEATURE: ; PEATURE: ; OTHER INFORMATION: Description of Artificial Sequence: Homo sapiens mutation US-09-880-137-7
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US-09-800-137A-4
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-800-137A-4
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US-09-800-137A-7
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TITLE OF INVENTION: METHODS OF ASSAYING FOR G
TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
FILE REFERENCE: MNI-131
CURRENT APPLICATION NUMBER: US/09/880,137
CURRENT FILING DATE: 2001-03-05
PRIOR APPLICATION UMBER: US 60/186,706
PRIOR PRILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 409
TYPE: DEF
              Sequence 7, Application US/09800137A

Publication No. US20030157553A1

GENERAL INFORMATION:

APPLICANT: Berstein, Gabriel
TITLE OF INVENTION: METHODS OF ASSAVING FOR G
TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
FILE REFERENCE: MNI-131

CURRENT APPLICATION NUMBER: US/09/800,137A

CURRENT APPLICATION NUMBER: US/09/800,137A

CURRENT FILING DATE: 2000-03-03

PRIOR APPLICATION NUMBER: US/09/800,137A

CURRENT FILING DATE: 2000-03-03

NUMBER OF SEQ ID NOS: 8

NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/800,137A
CURRENT FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: US 60/186,706
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/09800137A
Publication No. US20030157553A1
GENERAL INFORMATION:
APPLICANT: Berstein, Gabriel
TITLE OF INVENTION: METHODS OF ASSAYING FOR G
TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
FILE REFERENCE: MNI-131
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Best Local Similarity 100.0%; P
Matches 11; Conservative 0;
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Best Local Similarity 100.0%;
Matches 11; Conservative (
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SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No.
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Pred. No.
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; LENGTH: 409; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Homo sapiens mutation US-09-800-137A-7
Search completed: May 20, 2006, 23:30:49 Job time: 182 secs
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                                                                                                                                Query Match 2.9%;
Best Local Similarity 100.0%;
Matches 11; Conservative (
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                                                                    339 ELPEVIMHPKP
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                                                                                                                                   Score 11; DB 3; pred. No. 0.16; O; Mismatches
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Match Length
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| EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
| EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
| EMC_Celerra_SIDS3/ptodata/2/pubpaa/US31_NEW_PUB.pep:*
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        US-10-505-928-173
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US-11-258-767-17
US-11-258-767-19
US-11-258-767-21
US-11-258-767-30
US-11-258-767-30
US-11-258-767-34
US-10-511-937-2463
US-10-511-937-2463
US-10-511-937-2437
US-10-106-014-50
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US-10-505-928-173
; Sequence 173, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
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ALIGNMENTS

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Sequence 31, Application US/11258767

; Beduence 31, Application US/20060094082A1

; GENERAL INFORMATION:
APPLICANT: Varadhachary, Atul
APPLICANT: Glynn, Peter
; APPLICANT: Betrak, Karel
APPLICANT: Engelmayer, Jose
TITLE OF INVENTION: COMPOSITIONS OF LACTOFERRIN RELATED PEPTIDES AND USES THEREOF
FILE REFERENCE: HO-P02915US1
CURRENT APPLICATION NUMBER: US/11/258,767
; CURRENT APPLICATION NUMBER: US/11/258,767
; CURRENT FILING DATE: 2004-10-26
; PRIOR FILING DATE: 2004-10-26
; NUMBER OF SEQ ID NOS: 67
; SOCTWARE: Patentin version 3.3
; SEQ ID NO 31
LENGTH: 709
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SOFTWARE: PatentIn 3.2
SEQ ID NO 173
LENGTH: 409
TYPE: PRT
ORGANISM: Homo sapiens
US-10-505-928-173
                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 2
US-11-258-767-31
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CURRENT APPLICATION NUMBER: US/10/505,928
CURRENT FILING DATE: 2004-08-27
PRIOR APPLICATION NUMBER: US 60/363,019
PRIOR FILING DATE: 2002-03-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             339 ELPFVLMHPKP 349
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; TYPE: PRT
; ORGANISM: HUMAN
US-11-258-767-33
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US-11-258-767-33
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; ORGANISM: HUMAN
US-11-258-767-12
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                                                                                                                                                                                                                                                                                                    APPLICANT: Varadhachary, Atul
APPLICANT: Glynn, Peter
APPLICANT: Glynn, Peter
APPLICANT: Betrak, Karel
APPLICANT: Engelmayer, Jose
TITLE OF INVENTION: COMPOSITIONS OF LACTOFERRIN RELATED PEPTIDES AND USES THEREOF
FILE REFERENCE: HO-P02915US1
CURRENT APPLICATION NUMBER: US/11/258,767
CURRENT FILING DATE: 2005-10-26
PRIOR APPLICATION NUMBER: US 60/622,176
PRIOR APPLICATION NUMBER: US 60/622,176
PRIOR APPLICATION NUMBER: US 60/622,176
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TITLE OF INVENTION: COMPOSITIONS OF LACTOFERRIN RELATED PEPTIDES AND USES THEREOF
FILE REFERENCE: HO-P02915US1
CURRENT APPLICATION NUMBER: US/11/258,767
CURRENT FILING DATE: 2005-10-26
PRIOR APPLICATION NUMBER: US 60/622,176
PRIOR FILING DATE: 2004-10-26
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin version 3.3
SEQ ID NO 33
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Publication No. US20060094082A1
GENERAL INFORMATION:
                                                                                Query Match 1.8%; Score 7; DB 7; Best Local Similarity 100.0%; Pred. No. 8.3; Matches 7; Conservative 0; Mismatches
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1.8%; Score 7; DB Gest Local Similarity 100.0%; Pred. No. 8.:
Matches 7; Conservative 0; Mismatches
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APPLICANT: Glynn, Peter
APPLICANT: Petrak, Karel
APPLICANT: Engelmayer, Jose
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                       329 LFLGALG 335
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                    RESULT 7
US-11-258-767-18
; Sequence 18, Application US/11258767
; Publication No. US20060094082A1
; GENERAL INFORMATION:
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US-11-258-767-15
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; ORGANISM: HUMAN
US-11-258-767-15
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CURRENT APPLICATION NUMBER: US/11/258,767
COURRENT FILING DATE: 2005-10-26
PRIOR APPLICATION NUMBER: US 60/622,176
PRIOR FILING DATE: 2004-10-26
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin version 3.3
SEQ ID NO 17
LENGTH: 711
TYPE: PRT
ORGANISM: HUMAN
US-11-258-767-17
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Best Local Similarity
Thes 7; Conserva
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APPLICANT: Glynn, Peter
APPLICANT: Glynn, Peter
APPLICANT: Engelmayer, Jose
TITLE OF INVENTION: COMPOSITIONS OF LACTOFERRIN RELATED PEPTIDES AND USES THEREOF
FILE REFERENCE: HO-P02915US1
CURRENT APPLICATION NUMBER: US/11/258,767
CURRENT FILING DATE: 2005-10-26
PRIOR APPLICATION NUMBER: US 60/622,176
PRIOR APPLICATION NUMBER: US 60/622,176
PRIOR FILING DATE: 2004-10-25
SOFTWARE: Patentin version 3.3
SEQ ID NO 15
LENGTH: 711
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Publication No. US20060094082A1
GENERAL INFORMATION:
                                                    Query Match 1.8%; Score 7; DB 7; Best Local Similarity 100.0%; Pred. No. 8.3; Matches 7; Conservative 0; Mismatches
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APPLICANT: Glynn, Peter
APPLICANT: Petrak, Karel
APPLICANT: Engelmayer, Jose
329 LFLGALG 335
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100.0%; Pred. No. 8.:
tive 0; Mismatches
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; LENGTH: 711
; TYPE: PRT
; ORGANISM: HUMAN
US-11-258-767-18
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; SEQ ID NO 21
; LENGTH: 711
; TYPE: PRT
; ORGANISM: HUMAN
US-11-258-767-21
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TITLE OF INVENTION: COMPOSITIONS OF LACTOFERRIN RELATED PEPTIDES AND USES THEREOF
FILE REFERENCE: HO-P02915US1
CURRENT APPLICATION NUMBER: US/11/258,767
CURRENT FILING DATE: 2005-10-26
PRIOR APPLICATION NUMBER: US 60/622,176
PRIOR APPLICATION NUMBER: US 60/622,176
PRIOR FILING DATE: 2004-10-26
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin version 3.3
SEQ ID NO 18
                                                                                                                                                                                            Sequence 27, Application US/11258767 Publication No. US20060094082A1 GENERAL INFORMATION:
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Best Local :
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APPLICANT: Varadhachary, Atul
APPLICANT: Glynn, Peter
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Matches 7; Conserva
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TITLE OF INVENTION: COMPOSITIONS OF LACTOFERRIN RELATED PEPTIDES AND USES THEREOF
FILE REFERENCE: HO-P02915US1
CURRENT APPLICATION NUMBER: US/11/258,767
CURRENT FILING DATE: 2005-10-26
PRIOR APPLICATION NUMBER: US 60/622,176
PRIOR PILING DATE: 2004-10-26
PRIOR FILING DATE: 2004-10-26
PRIOR FILING DATE: 2004-10-26
NUMBER OF SEQ ID NOS: 67
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             APPLICANT: Varadhachary, Atul
APPLICANT: Glynn, Peter
APPLICANT: Glynn, Peter
APPLICANT: Petrak, Karel
APPLICANT: Engelmayer, Jose
TITLE OF INVENTION: COMPOSITIONS OF LACTOFERRIN RELATED PEPTIDES AND USES THEREOF
FILE REFERENCE: HO-P02915US1
CURRENT APPLICATION NUMBER: US/11/258,767
CURRENT FILING DATE: 2005-10-26
CURRENT FILING DATE: 2005-10-26
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RIOR APPLICATION NUMBER: US 60/622,176
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Petrak, Karel
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100.0%; Pred. No. 8.3;
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CURRENT APPLICATION NUMBER: US/11/258,767;
CURRENT FILING DATE: 2005-10-26
PRIOR APPLICATION NUMBER: US 60/622,176
PRIOR FILING DATE: 2004-10-26
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin version 3.3
SEQ ID NO 30
LENGTH: 711
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Best Local Similarity
Thes 7; Conserva
APPLICANT: Engelmayer, Jose
TITILE OF INVENTION: COMPOSITIONS OF LACTOFERRIN RELATED PEPTIDES AND USES THEREOF
FILL REFERENCE: HO-P02915US1
CURRENT APPLICATION NUMBER: US/11/258,767
CURRENT FILING DATE: 2005-10-26
PRIOR FILING DATE: 2004-10-26
PRIOR APPLICATION NUMBER: US 60/622,176
PRIOR FILING DATE: 2004-10-26
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin version 3.3
SEQ ID NO 34
LENGTH: 711
TYPE: PRT
IORGANISM: HUMAN
US-11-258-767-34
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US-11-258-767-34
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; ORGANISM: HUMAN
US-11-258-767-30
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; Sequence 30, Application US/11258767
; Publication No. US20060094082A1
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; ORGANISM: HUMAN
US-11-258-767-27
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NUMBER OF SEQ ID NOS: 67
SOFTWARE: PatentIn version 3.3
SEQ ID NO 27
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APPLICANT: Varadhachary, Atul
APPLICANT: Glynn, Peter
APPLICANT: Petrak, Karel
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APPLICANT: Varadhachary, Atul
APPLICANT: Glynn, Peter
APPLICANT: Petrak, Karel
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TITLE OF INVENTION: COMPOSITIONS OF LACTOFERRIN RELATED PEPTIDES AND USES
FILE REFERENCE: HO-P02915US1
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100.0%; Pred. No.
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PRIOR APPLICATION NUMBER: PCT/US2003/012946
PRIOR FILING DATE: 2003-04-24
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR APPLICATION NUMBER: US 10/325,899
PRIOR APPLICATION NUMBER: US 10/325,899
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: Patentin version 3.2
SEQ ID NO 2463
LENGTH: 993
TYPE: PRT
ORGANISM: Homo sapiens
US-10-511-937-2463
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US-10-706-435A-24
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SEQ ID NO 24
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Best Local
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Best Local :
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Publication No. US20060088836A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
               APPLICANT: Angov, Evelina
APPLICANT: Kumar, Sanjai
APPLICANT: Rogers, William
APPLICANT: Barbosa, Arnoldo
TITLE OF INVENTION: Expression, Purification, and Uses of a Plasmodium
TITLE OF INVENTION: Ediciparum Liver Stage Antigen 1 Polypeptide
FILE REFERENCE: 003/285/SAP
CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: US/10/706,435A
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: 60/425,719
PRIOR FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Microsoft Word XP
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                                                                                                                                                                                                                                                                   APPLICANT: Walter Reed Army Institute APPLICANT: Lanar, David E. APPLICANT: Hillier, Collette J. APPLICANT: Lyon, Jeffrey A. APPLICANT: Lyon, Jeffrey A. APPLICANT: Angov, Evelina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Morris, MacDonald
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
FILE REFERENCE: 506612000104
CURRENT PEPLICATION NUMBER: US/10/511,937
CURRENT FILING DATE: 2004-10-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: EXPRESSION DIAGNOSTICS, INC. APPLICANT: Wohlgemuth, Jay
APPLICANT: Fry, Kirk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h 1.8%; Score 7; DB (Similarity 100.0%; Pred. No. 12.7; Conservative 0; Mismatches
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Prentice, James
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100.0%; Pred. No. 8.
tive 0; Mismatches
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APPLICANT: TBAI, FORGATION: NOVEL 13237, 18480, 2245, 16228, 7677, TITLE OF INVENTION: NOVEL 13237, 18480, 2245, 16228, 7677, TITLE OF INVENTION: 26320, 46619, 33166, 16836, 46867, 21617, 5556, TITLE OF INVENTION: 26208, 46745, 23155, 21557, 42755, 32229, 2233

TITLE OF INVENTION: 32252 MOLECULES AND USES THEREFOR FILE REFERENCE: MPI03-0170MNIM
CURRENT APPLICATION NUMBER: US/10/370,959

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: US 69/910,150

PRIOR FILING DATE: 2001-07-18

PRIOR APPLICATION NUMBER: US 60/219,028

PRIOR FILING DATE: 2000-07-19

PRIOR PRIOR PRIOR DATE: 2000-07-19

PRIOR PRIOR PRIOR NUMBER: US 10/251,507

PRIOR PRIOR APPLICATION NUMBER: US 99/715,479

PRIOR PRIOR APPLICATION NUMBER: US 60/218,053

PRIOR APPLICATION NUMBER: US 60/218,053

PRIOR APPLICATION NUMBER: US 60/218,053

PRIOR PILING DATE: 2000-08-23

PRIOR PILING DATE: 2000-08-16

PRIOR PILING DATE: 2000-08-16

PRIOR PILING DATE: 2000-08-17
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                                                                                       ; ORGANISM: Artificial Sequence ; FEATURE: OTHER INFORMATION: Consensus amino acid US-10-370-959-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
US-10-370-959-30
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                                                                                                                                                                                                                              Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 156
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 30, Application US/10370959 Publication No. US20060088907A1
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APPLICANT: Meyers, Rachel E.
APPLICANT: Williamson, Mark W.
                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/214,174
PRIOR FILING DATE: 2000-06-26
PRIOR APPLICATION NUMBER: US 09/775,117
                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 09/892,870
PRIOR FILING DATE: 2001-06-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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ORGANISM: P. falciparum LSA-1
PEATURE:
OTHER INFORMATION: Amino acid sequence of LSA-NRC(H) repeat
OTHER INFORMATION: between N & C terminals
                                                                                                                                                                                       TYPE: PRT
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Hunter, John J.
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    Conservative
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100.0%; Pred. No.
                     1.6%; Score 6;
00.0%; Pred. No.
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APPLICANT: MORTIS, MacDonald
APPLICANT: MORTIS, MacDonald
APPLICANT: MORTIS, MacDonald
APPLICANT: MORTIS, METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
FILE REFERENCE: 506612000104
CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: PCT/US2003/012946
PRIOR FILING DATE: 2003-04-24
PRIOR FILING DATE: 2003-04-24
PRIOR FILING DATE: 2003-04-24
PRIOR FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR FILING DATE: 2002-04-24
PRIOR FILING DATE: 2002-04-24
PRIOR FILING DATE: 2002-04-24
PRIOR FILING DATE: 2002-01-20
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: PATENTIN VETSION 3.2
SEQ ID NO 2437
LENGTH: 142
TYPE: PAT
TYPE: PAT
TORGANISM: Homo. sapiens
US-10-511-937-2437
Search completed: May 20, 2006, 23:31:05 Job time : 10 secs
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Publication No. US20060088836A1
GENERAL INFORMATION:
                                                                                                                                                                                            Query Match 1.6%; Score 6; DB 6; Best Local Similarity 100.0%; Pred. No. 21; Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: EXPRESSION DIAGNOSTICS, INC.
APPLICANT: Wohlgemuth, Jay
APPLICANT: WOY, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
APPLICANT: Prentice, James
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                                                                                                16 KKLGSN 21
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